



O A 1 2 3 4 5 - Days p.i.

 = RIDβ

 = 14.7K

 = gp19K

a b c d e f g

FIGURE 29

0914241-070898

803020-1161160

gp19K

RID $\beta$

14.7K

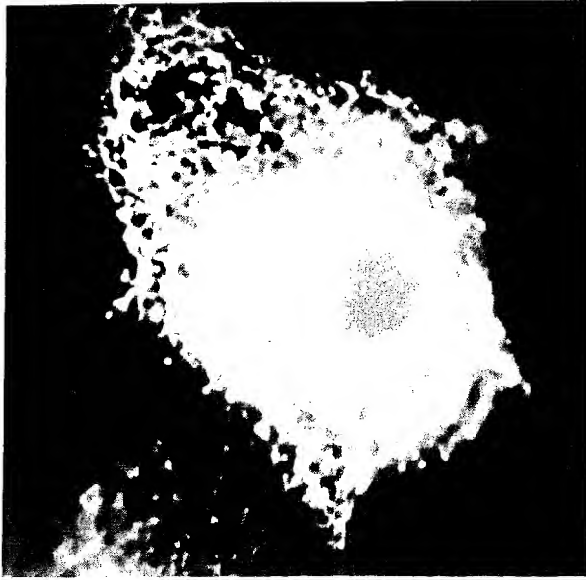


FIGURE 30A

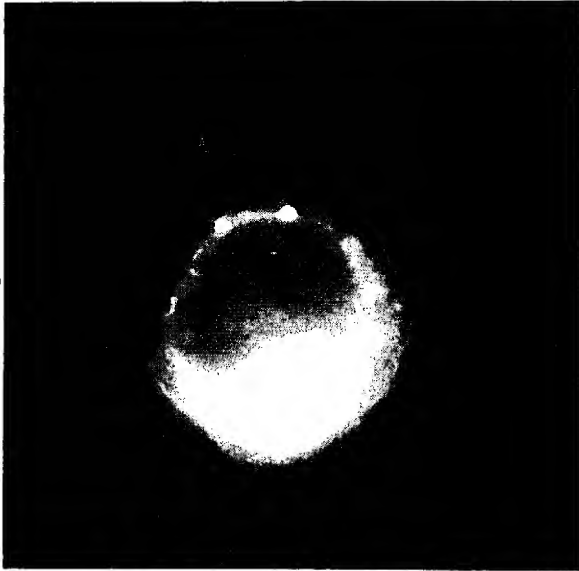


FIGURE 30B



FIGURE 30C

|          |     |   |     |
|----------|-----|---|-----|
| TNFR1    | 362 | V V E N V P P L R R W K E F V R R I G L S D H E I D R L E L Q N G R C L R E A Q Y | 401 |
| Fas      | 236 | I A G V M T L S Q V K G E F V R K N G V N E A K L D E I K N D N V Q D T A E Q K V | 275 |
| DR3      | 338 | V M D A V P A R R W K E F V R T I G L R E A E I E A V E V E I G R - F R D Q Q Y   | 376 |
| TRAIL-R1 | 348 | F A N I V P F D S W D Q L M R Q L D I T K N F E I D V V R A G T A G - P G D A L Y | 386 |
| TRAIL-R2 | 316 | F A D L V P F D S W E P L M R K E G L M D N E I K V A K A E A A G - H R D T L Y   | 354 |
| TNFR1    | 402 | S M L A T W R R R T P R R E A T L E L L G R V L R D M D L L G C L E D I E E       | 439 |
| Fas      | 276 | Q L L R N W H Q L H G K - K E A Y D T L L K D L K K A N L C T L A E K I Q T       | 313 |
| DR3      | 377 | E M L K R W R - - Q Q Q - P A G L G A V Y A A L E R M G L D G C V E D L R S       | 411 |
| TRAIL-R1 | 387 | A M L M K W V N K T G R - N A S I H T L L D A L E R M E E R H A K E K I Q D       | 423 |
| TRAIL-R2 | 356 | T M L I K W V N K T G R - D A S V H T L L D A L E T L G E R L A K Q K I E D       | 392 |

Figure 1

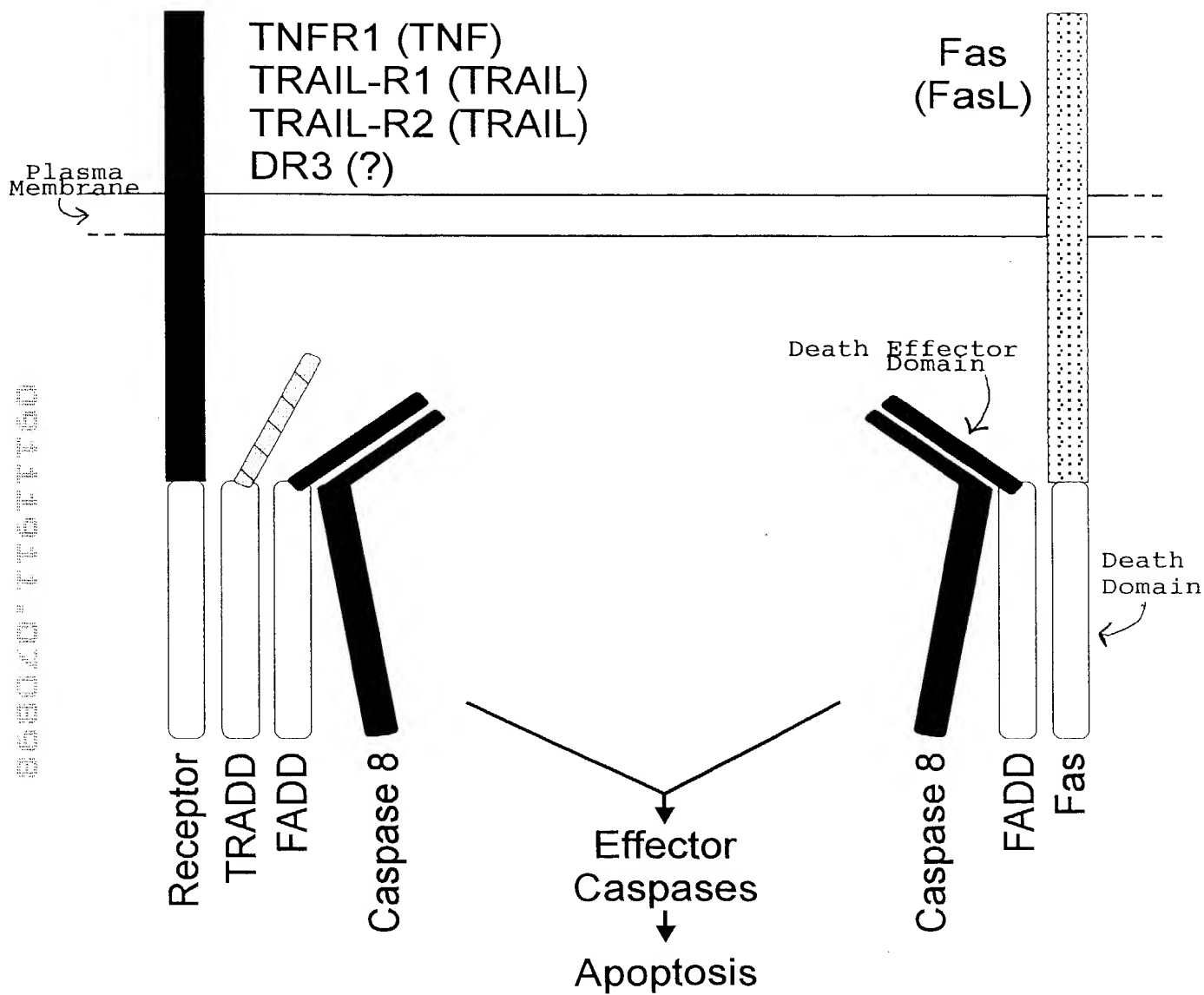


FIGURE 2

# RID COMPLEX

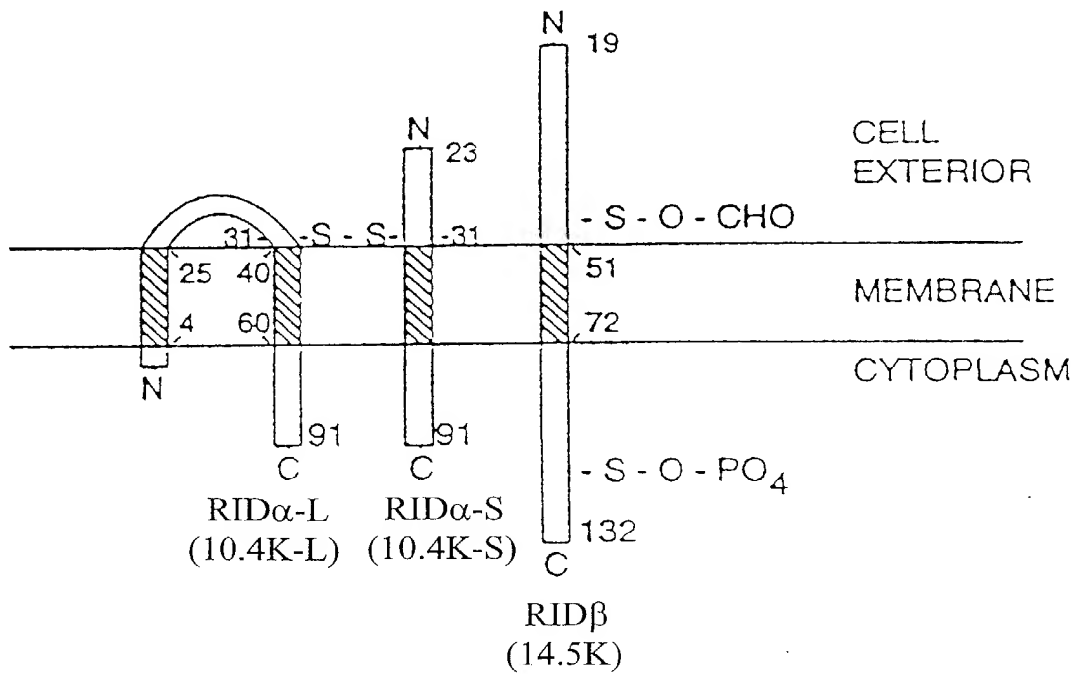


FIGURE 3

RID $\alpha$ -L (10.4K-L)

10 20  
M I P R V L I L L T L V A L F C A C S T L A A V A H I E  
signal sequence  
30 40 50  
V D C I P P F T V Y L L Y G F V T L I L I C S L V T V V  
\* transmembrane  
60 70 80  
I A F I Q F I D W V C V R I A Y L R H H P Q Y R D R T I  
90  
A D L L R I L

Figure 4A

RID $\alpha$ -S (10.4K-S)

10 20  
A V A H I E V D C I P P F T V Y L L Y G F V T L I L I C  
\* transmembrane  
30 40 50  
S L V T V V I A F I Q F I D W V C V R I A Y L R H H P Q  
60  
Y R D R T I A D L L R I L

Figure 4B

Pre-RID $\beta$  (14.5K)

```

          10                      20
M K F T V T F L L I I C T L S A F C S P T S K P Q R H I
  signal sequence

    30                      40                      50
S C R F T R I W N I P S C Y N E K S D L S E A W L Y A I

          60                      70                      80
I S V M V F C S T I L A L A I Y P Y L D I G W N A I D A
  Transmembrane

          90                      100                      110
M N H P T F P A P A M L P L Q Q V V A G G F V P A N Q P

          120                      130
R P P S P T P T E I S Y F N L T G G D D
      *                      *

```

Figure 4C

Mature-RID $\beta$  (14.5K)

```

          10                      20
S P T S K P Q R H I S C R F T R I W N I P S C Y N E K S

    30                      40                      50
D L S E A W L Y A I I S V M V F C S T I L A L A I Y P Y
  Transmembrane

          60                      70                      80
L D I G W N A I D A M N H P T F P A P A M L P L Q Q V V

          90                      100                      110
A G G F V P A N Q P R P P S P T P T E I S Y F N L T G G
                        *                      *

D D

```

Figure 4D



**FIGURE 25**





**FIGURE 24**

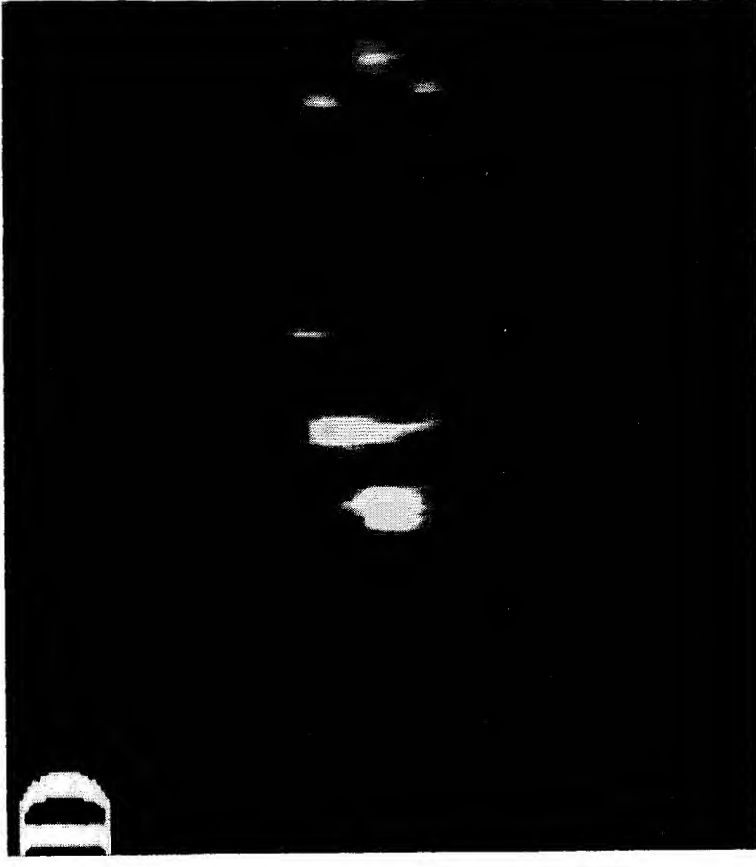
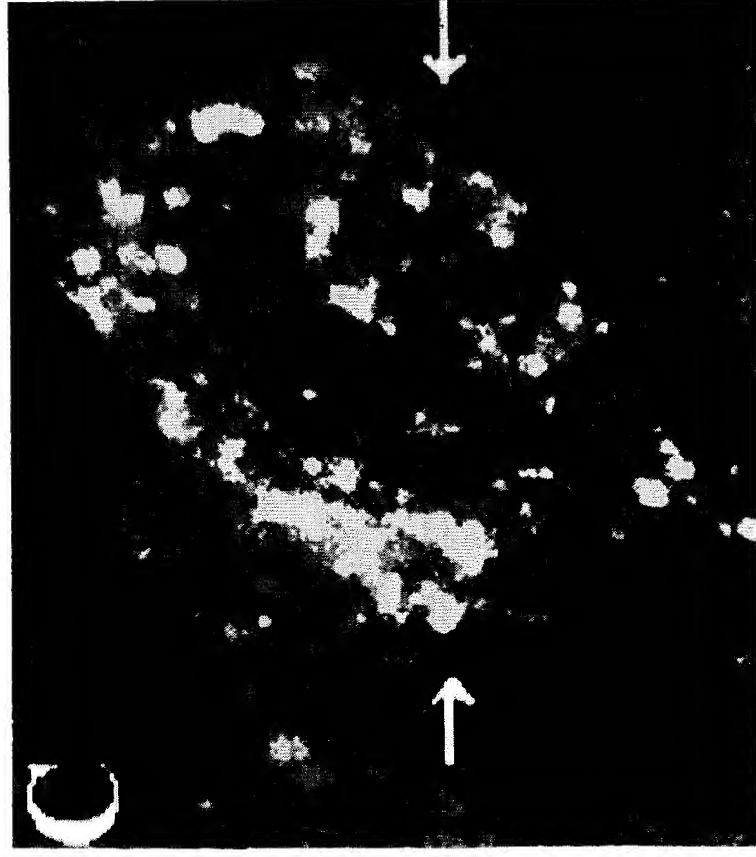
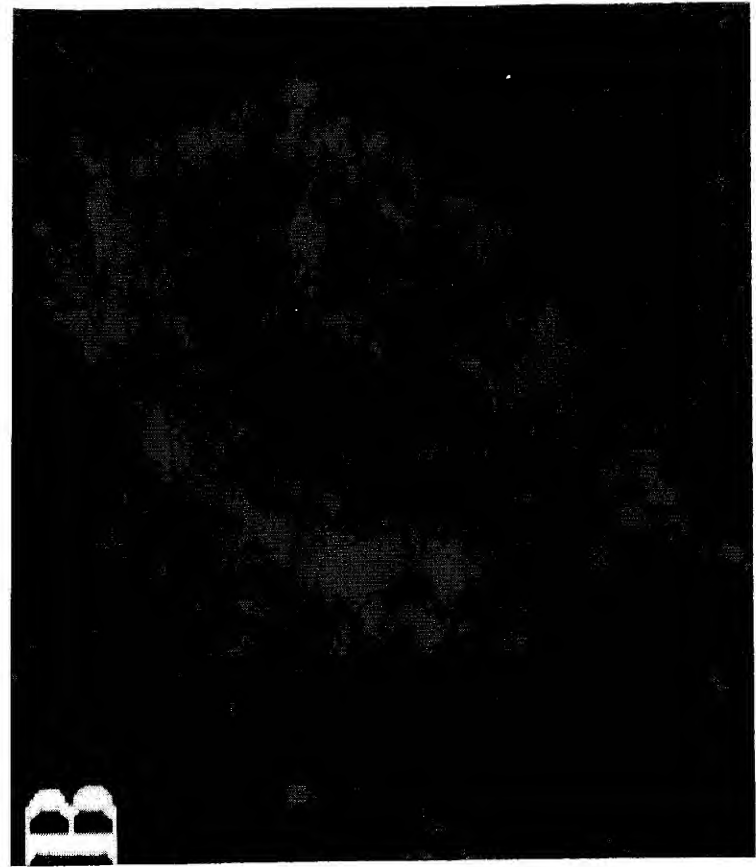


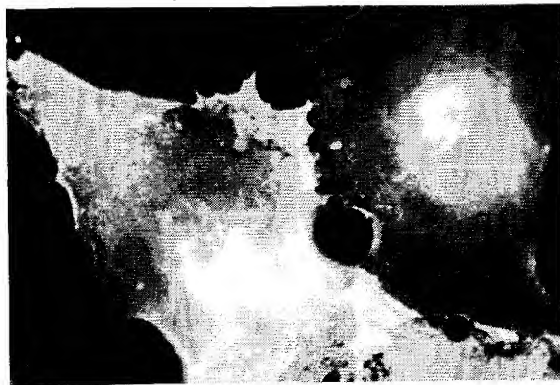
FIGURE 12

FIGURE 11

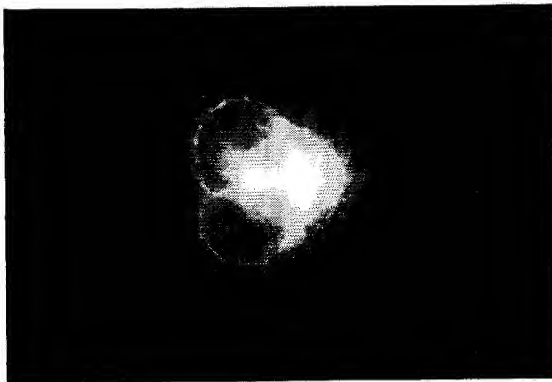
A. RID $\alpha$ , anti-RID $\alpha$



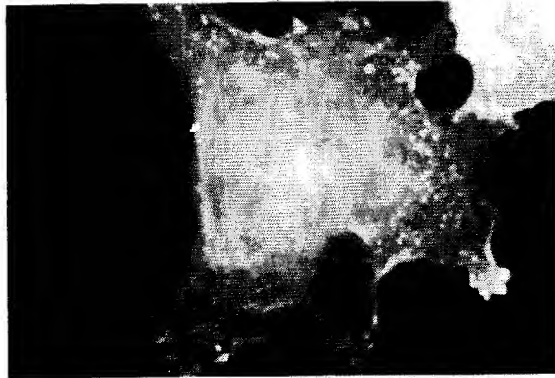
B. RID $\alpha$ , anti-Fas



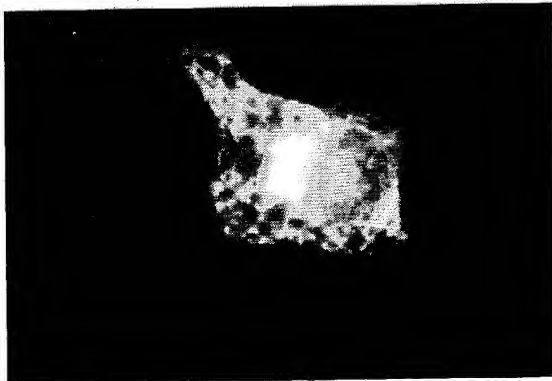
C. RID $\beta$ , anti-RID $\beta$



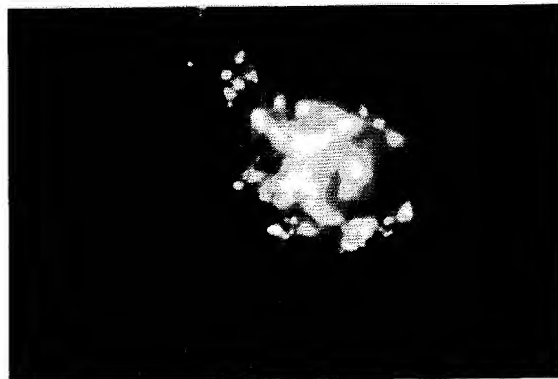
D. RID $\beta$ , anti-Fas



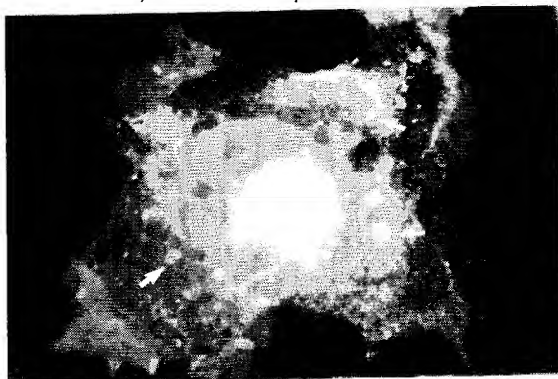
E. RID, anti-RID $\alpha$



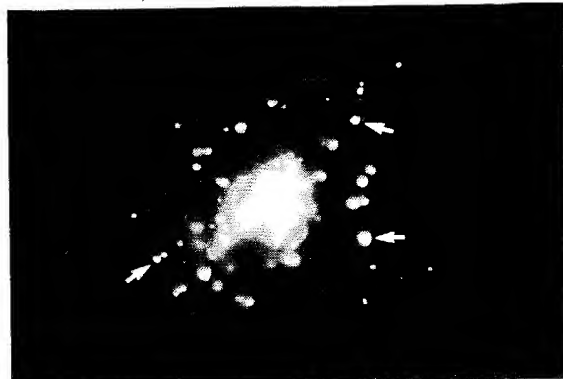
F. RID, anti-Fas



G. RID, anti-RID $\beta$



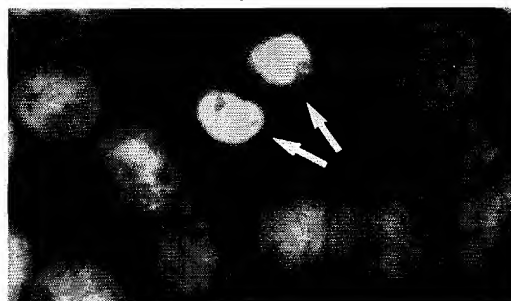
H. RID, anti-Fas



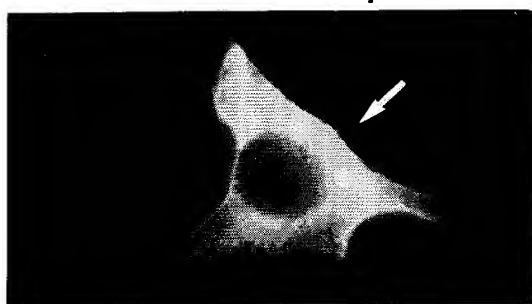
A. *rec700*, anti-DPB



B. *rec700*, DAPI



C. RID, anti-RID $\beta$



D. RID, DAPI

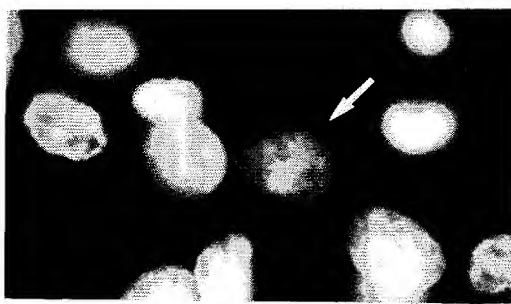
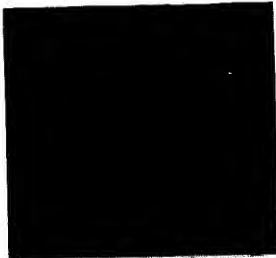


FIGURE 6

A. MCF7, Mock



B. MCF7-Fas, Mock



C. *rec700* (Wild Type)



D. *dl309* (RID<sup>-</sup>, 14.7K<sup>-</sup>)



E. *dl748* (RID $\alpha$ <sup>-</sup>, RID $\beta$ <sup>+</sup>)



F. *dl764* (RID $\alpha$ <sup>+</sup>, RID $\beta$ <sup>-</sup>)



G. *dl758* (RID<sup>+</sup>, 14.7K<sup>+</sup>)



H. *pm760* (RID $\uparrow$ )

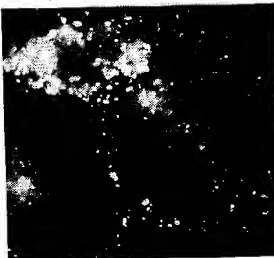


FIGURE 9

## FIGURE 5

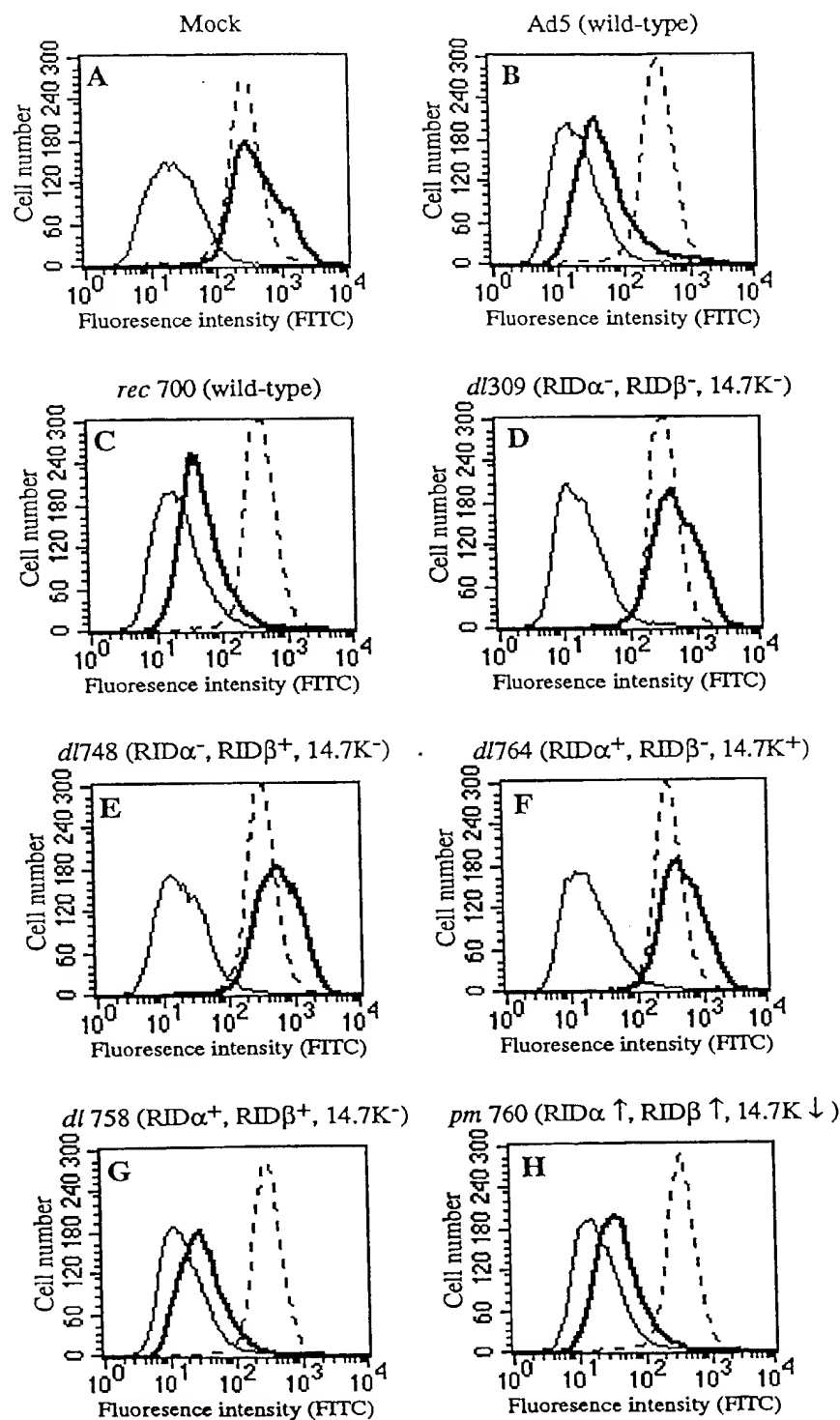
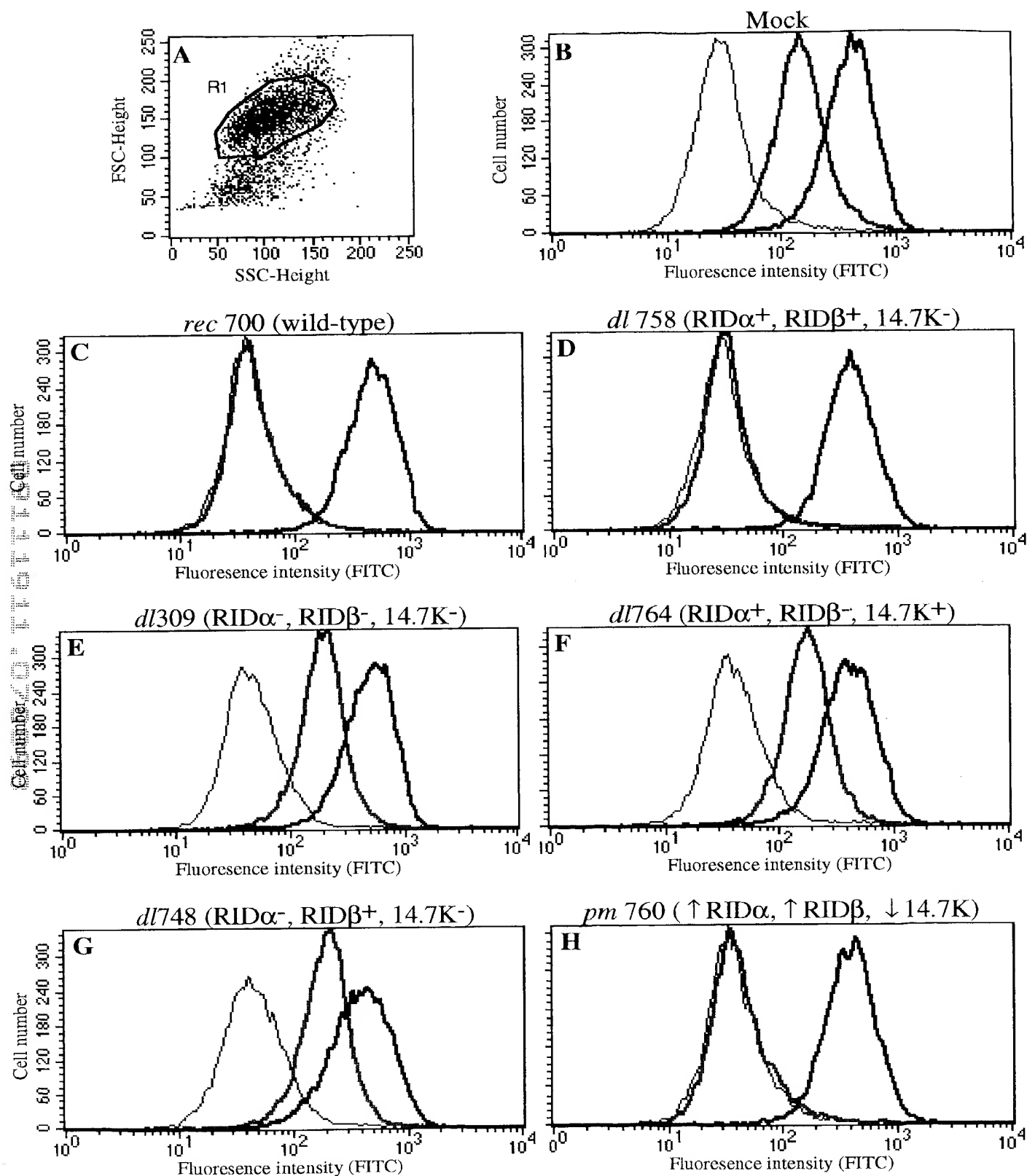


FIGURE 7



**FIGURE 8**



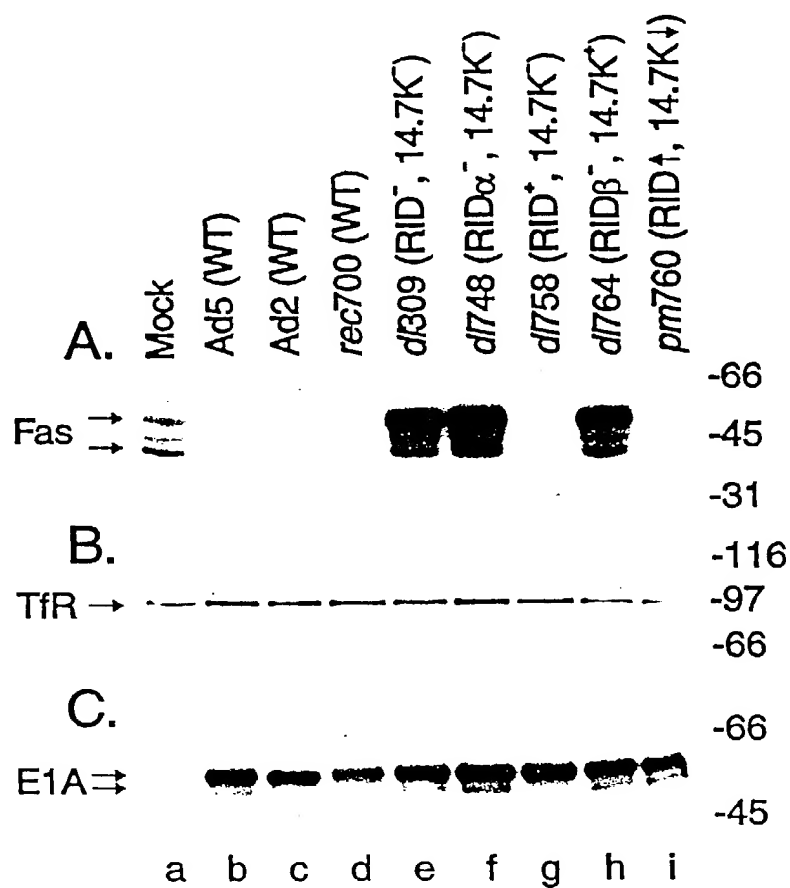
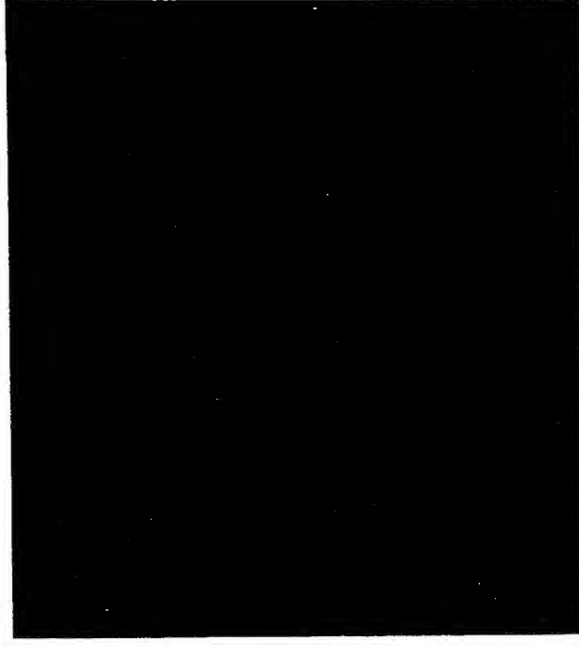
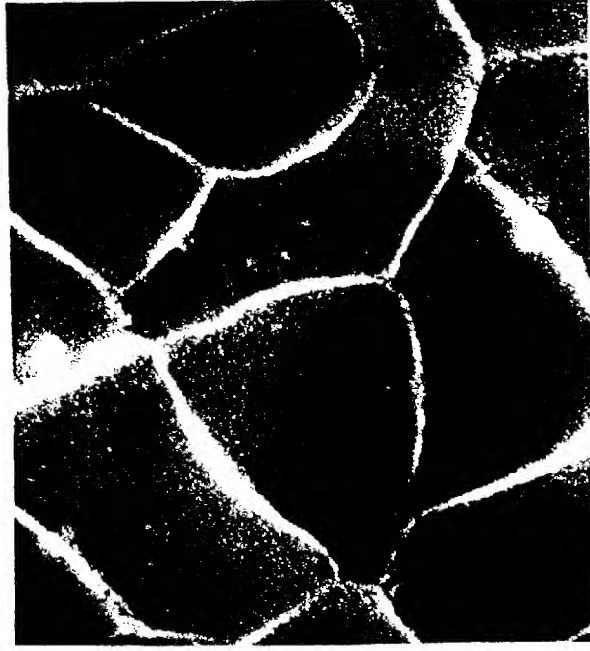


FIGURE 10

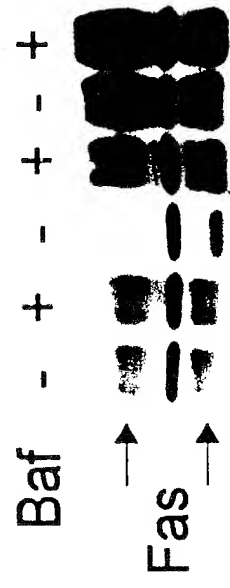
A *rec700* (WT), Baf<sup>+</sup> B *rec700* (WT), Baf<sup>-</sup>



C *d/309* (RID<sup>-</sup>), Baf<sup>+</sup>



D Mock 700 309



ERp72 →

E1B-19K →

FIGURE 13 a b c d e f

66003 T6 T60

|     | Mock 700  |   | 309 |   |   |   |
|-----|-----------|---|-----|---|---|---|
| Baf | -         | + | -   | + | - | + |
| TfR | — — — — — |   |     |   |   |   |

**FIGURE 13E**

094494.070899

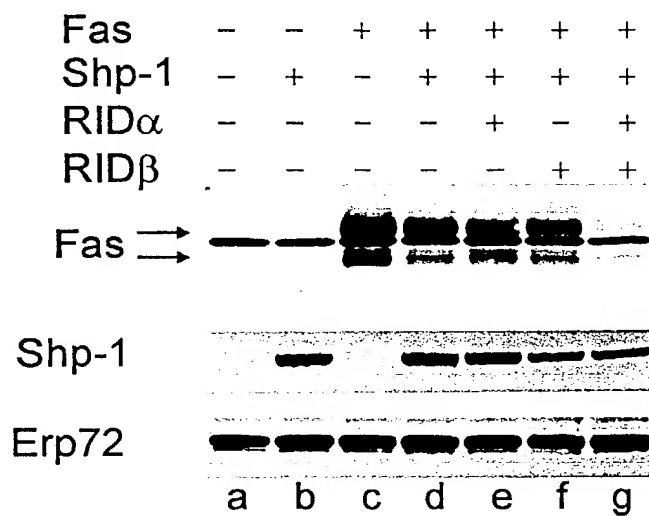
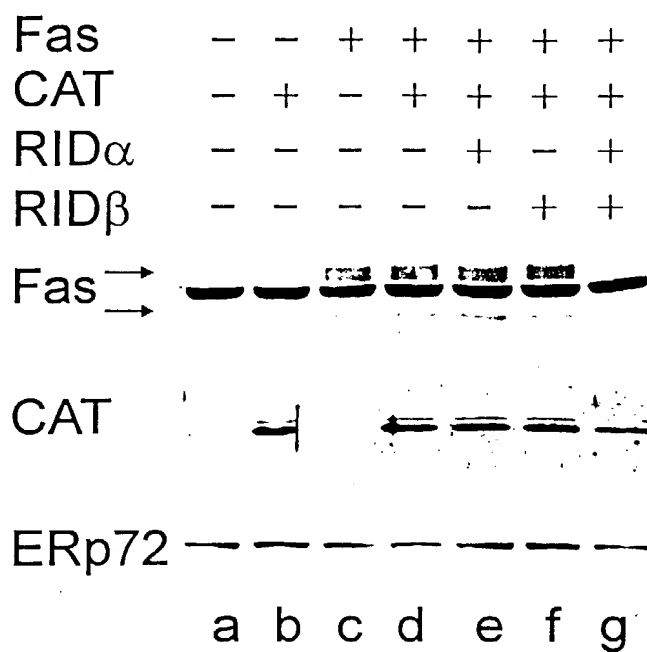


FIGURE 14



**FIGURE 15**



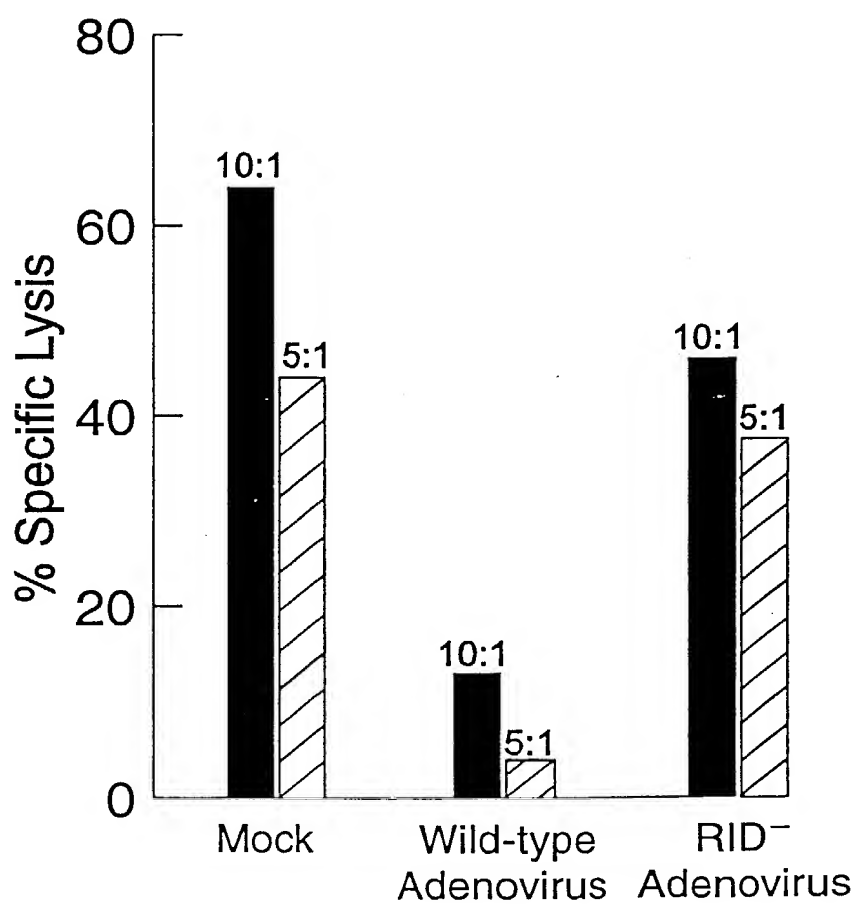
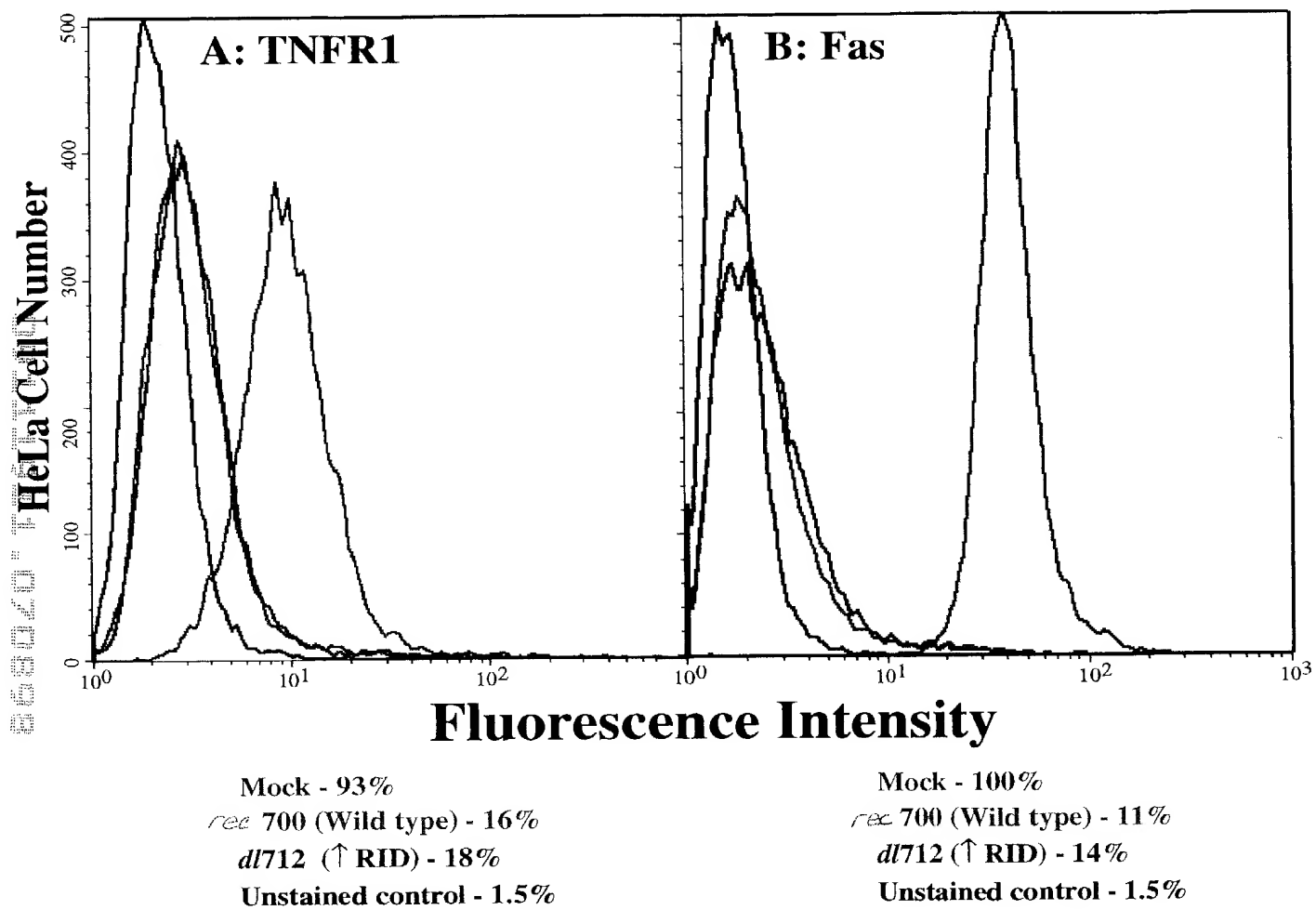


FIGURE 17



**FIGURE 18**



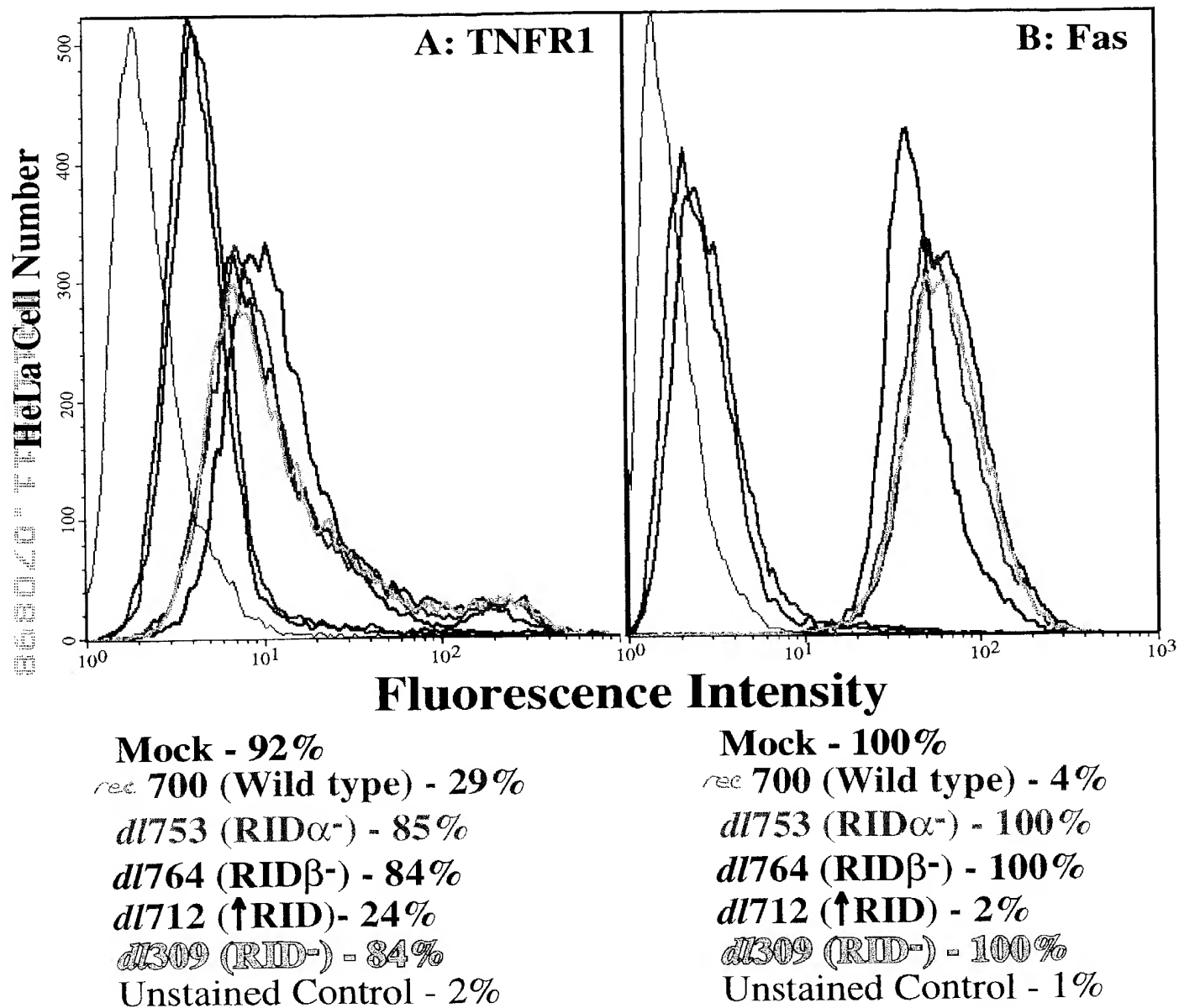
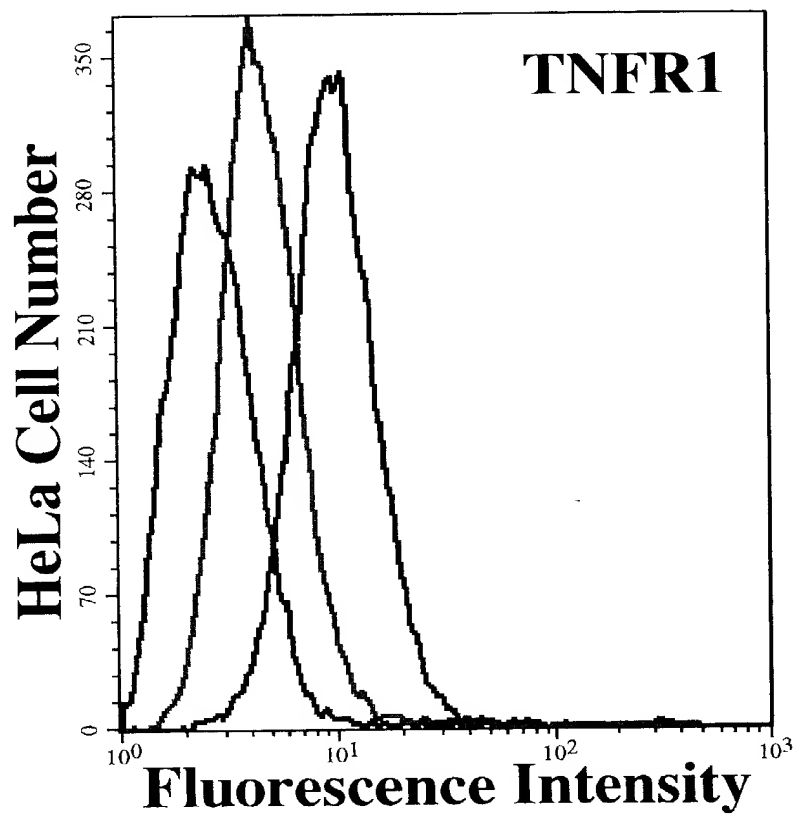


FIGURE 19

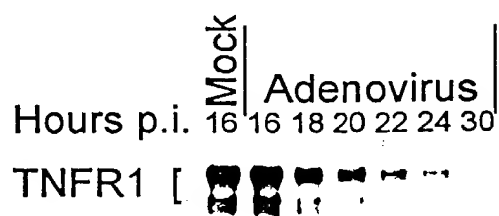


**Mock - 93%**

**231-10 (E3<sup>+</sup> vector) 24 hr. p.i. - 35%**

**231-10 (E3<sup>+</sup> vector) 48hr. p.i. - 11%**

**FIGURE 20**



**FIGURE 21**

09191107089

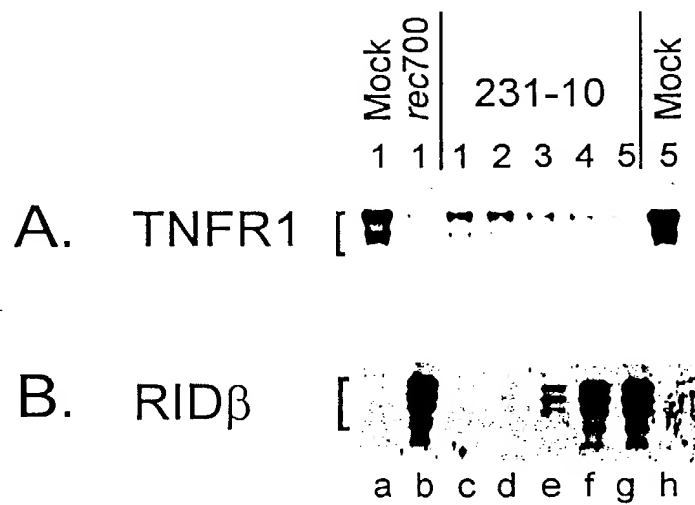
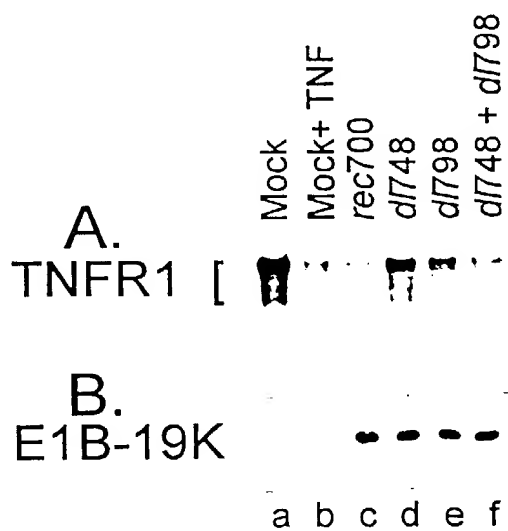


FIGURE 22



**FIGURE 23**

001491 0000

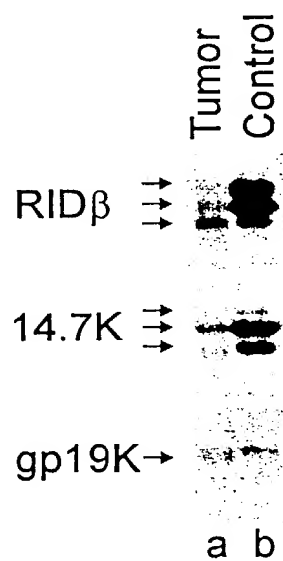
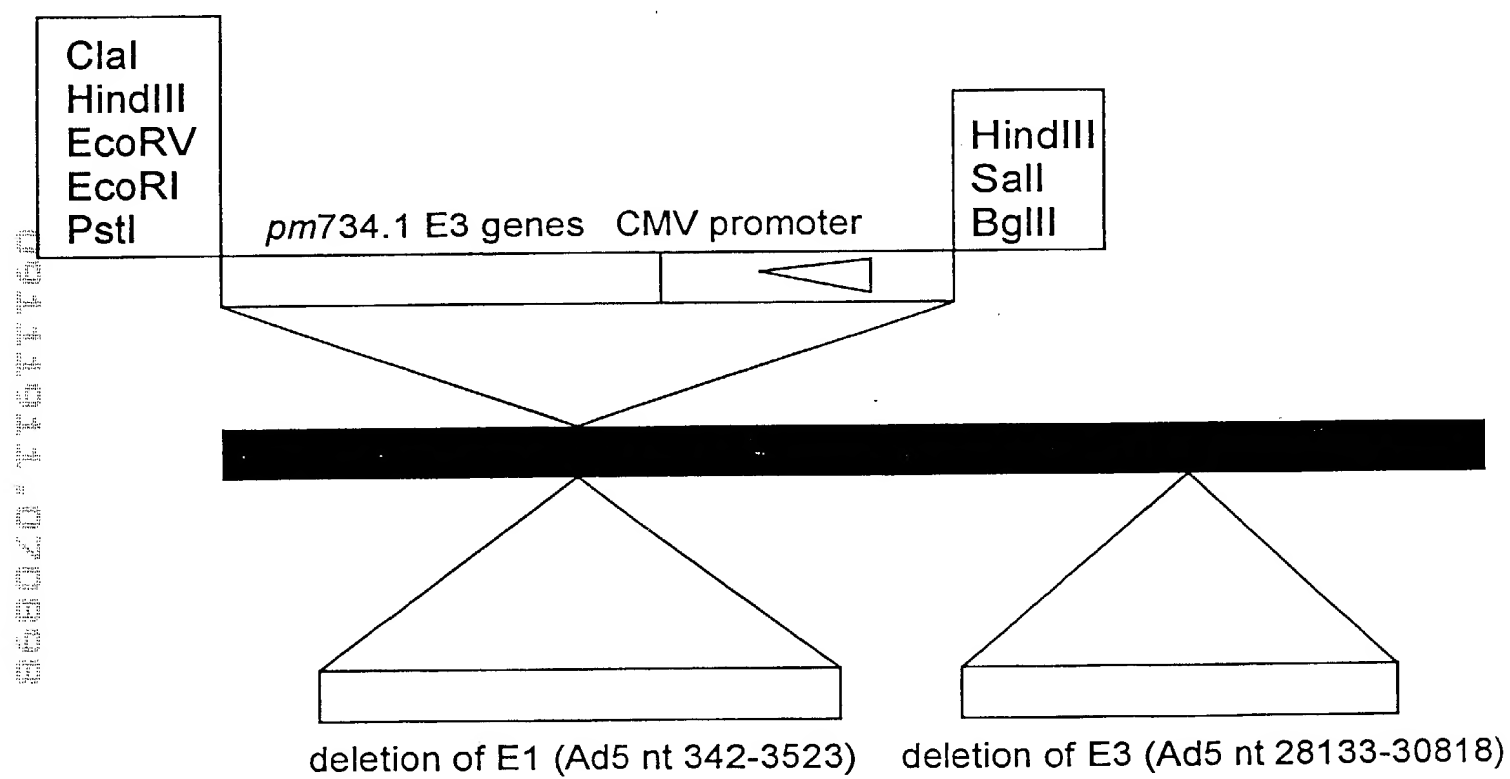


FIGURE 26



**FIGURE 27**

1 catcatcaataataaccttatttttgattgaagccaatatgataatgaggggtggagt 60  
 gtagtagttattatatggaataaaacctaacttcggttatactattactccccacctca  
 61 ttgtgacgtggcgcgggcggtgggaacggggcggtgacgtagtagtggtggcggaagtgt 120  
 aacactgcaccgcgccccgcacccttgccccgccactgcatcatcacaccgccttcaca  
 121 gatgttgcaagtgtggcggaacacatgtaagcgacggatgtggcaaaagtgcgtttttg 180  
 ctacaacgttcacacgccttggtgtacattcgctgcctacaccgttttcactgcaaaaac  
 181 gtgtgcgcgggtgtacacaggaagtgcacaattttcgcgcggttttagcggtgtgttag 240  
 cacacgcgggccacatgtgtccttcactgttaaagcgcgccaaaatccgcctacaacatc  
 241 taaatttggcgtaaccgagtaagatttggccattttcgcgggaaaactgaataagagga 300  
 atttaaacccgcattggctcattctaaaccggtaaaagcgcccttttgacttattctcct  
 301 agtgaaatctgaataattttgtgttactcatagcgcgtaatatcgataagcttgatatcg 360  
 tcacttttagacttattaaaacacaatgagtatcgcgcatatagctattcgaaactatagc  
 361 aattcctgcagccctatggatacacggggttgaaggatcttcagacgggtcttgcgcgct 420  
 ttaaggacgtcgggatacctatgtgccccaaacttccatagaagtctgccagaacgcgcga  
 421 tcactctgcaacaacatgaagatagtggtgctggatggacaggaacaggaggaaactgaca 480  
 agtagacgttgtgtacttctatcacccacgcctacctgtccttgcctcctttgactgt  
 481 ttccatttagattgtggagaaagtttgcagccaggaggaagctgcaataaccagagctggg 540  
 aaggtaaatctaacacctctttcaaacgtcggtcctccttcgacgttatggtctcgaccc  
 541 aggagggaaggaggtgctgctgaataaaactggacagaaatttgtaactgattttaagt 600  
 tcctcccggttctccacgacgacttatttgacctgtcttttaaacgattgactaaaattca  
 601 aagtgatgctttattattttttttattagtttaaagggaataagatctttgagaccgcac 660  
 ttcactacgaaataataaaaaaaataatcaatttcccttattctagaaaactctggcggtg

Restriction sites indicated above the sequence:  
 EciI (position 100)  
 AflIII, BspLU111, EciI, NspI (position 130)  
 BsrGI, BsrFI, SgrAI, TatI, EciI (position 190)  
 HaeI, MscI, EaeI (position 250)  
 ApoI (position 250)  
 HindIII, ClaI, ApoI, EcoRI, EcoRV (position 320)  
 BciVI, PstI, SfcI, Eco57I, BssHII (position 380)  
 TaqII (position 450)  
 XcmI, AceIII (position 510)  
 BseRI, BspGI, ApoI (position 570)  
 BsaI, BglII, BstYI, HgiEII (position 630)

FIGURE 28



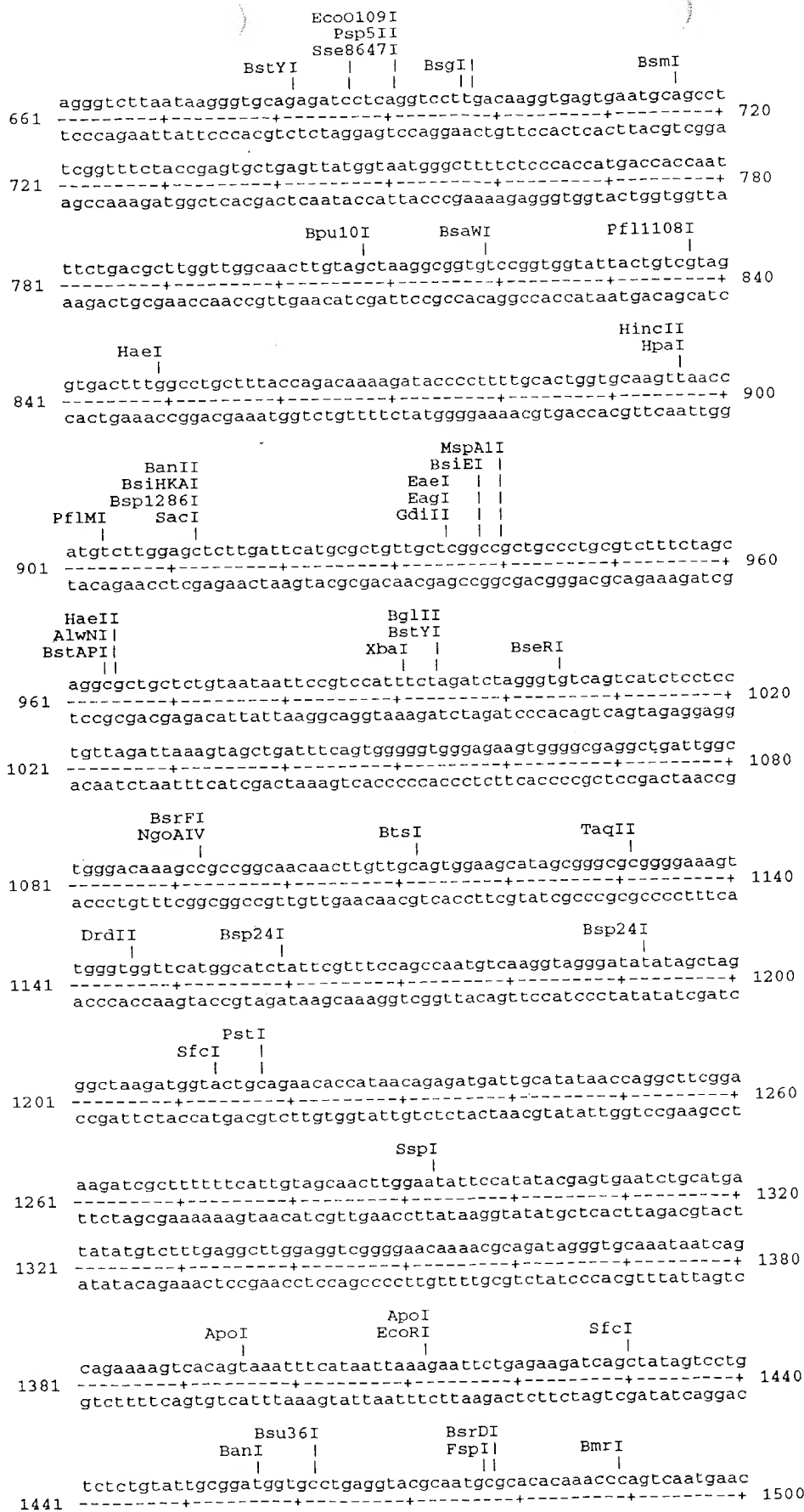


FIGURE 28

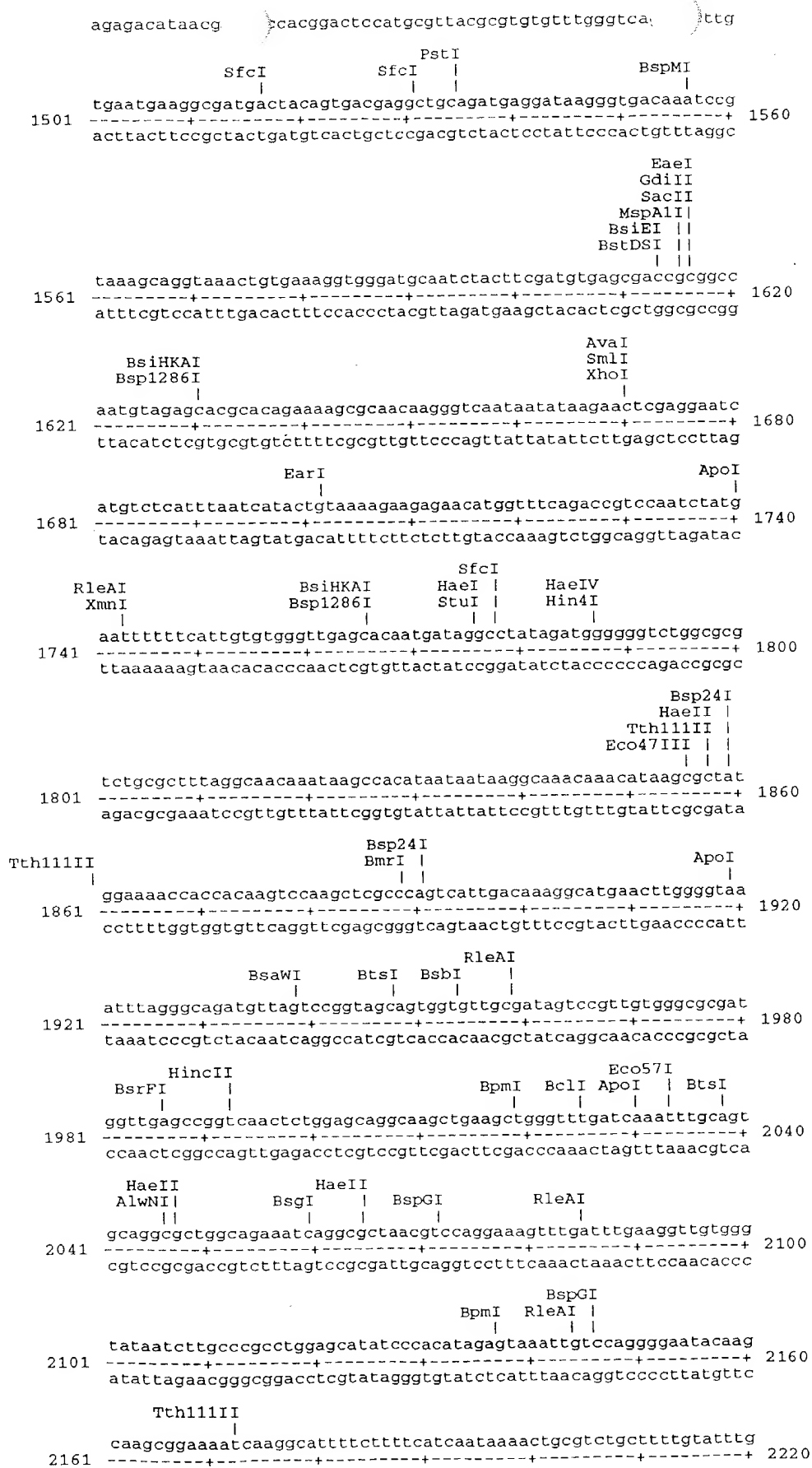


FIGURE 28





FIGURE 28

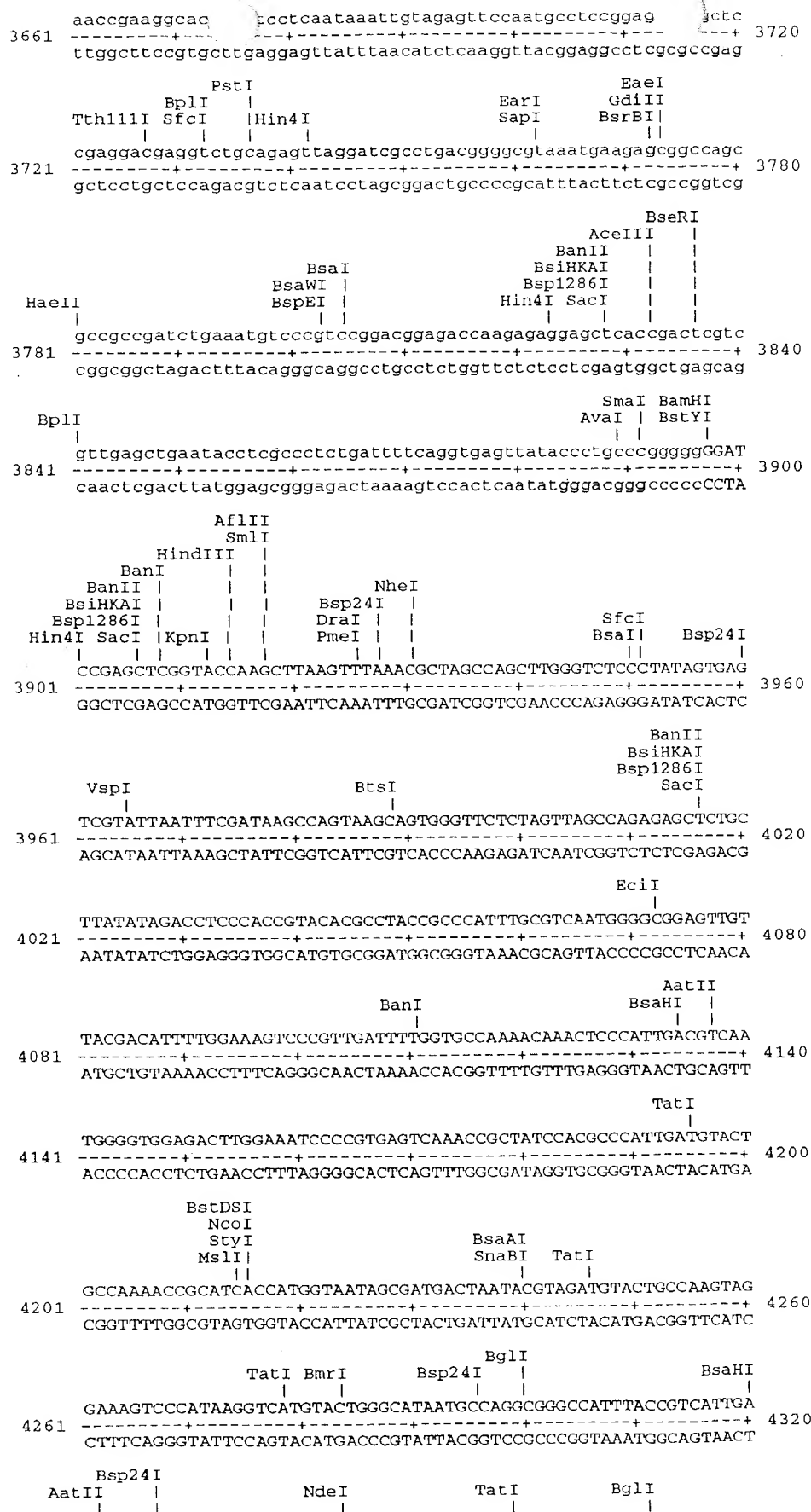


FIGURE 28

CGTCAATAGGGG ACTTGGCATATGATACACTTGATGTACTGCCAAGTG TTTT  
 4321 -----+-----+-----+-----+-----+-----+-----+ 4380  
 GCAGTTATCCCCCGCATGAACCGTATACTATGTGAAC TACATGACGGTTCACCCGTCAAA

TaqII  
 AatII  
 BsaHI

ACCGTAAATAGTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAA  
 4381 -----+-----+-----+-----+-----+-----+ 4440  
 TGGCATTATCAGGTGGGTAAC TGCAGTTACCTTTCAGGGATAACCGCAATGATACCTT

AatII  
 BsaHI BglI

CATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCAT  
 4441 -----+-----+-----+-----+-----+-----+ 4500  
 GTATGCAGTAATAACTGCAGTTACCCGCCCCCAGCAACCCGCCAGTCGGTCCGCCCGTA

TTACCGTAAGTTATGTAACGCGGAAC TCCATATATGGGCTATGAACTAATGACCCCGTAA  
 4501 -----+-----+-----+-----+-----+-----+ 4560  
 AATGGCATTCAATACATTGCGCCTTGAGGTATATACCCGATACTTGATTACTGGGGCATT

AflIII  
 MluI  
 HincII  
 VspI SpeI

TTGATTACTATTAACTAGTCAATAATCAATGTCAACGCGTATATCTGGCCCGTACAT  
 4561 -----+-----+-----+-----+-----+-----+ 4620  
 AACTAATGATAATTATTGATCAGTTATTAGTTACAGTTGCGCATATAGACCGGGCATGTA

HincII  
 Bsp24I  
 AccII  
 NruI Bpu10I HindIII SalI

CGCGAAGCAGCGCAAAACGCCTAACCCTAAGCAGATTCTTCATGCAATTcaagcttgtcg  
 4621 -----+-----+-----+-----+-----+-----+ 4680  
 GCGCTTCGTCGCGTTTTCGCGGATTGGGATTTCGTCTAAGAAAGTACGTTAagttcgaacagc

Bsp24I  
 BglII  
 BstYI AflIII  
 SmlI

acagatcttgggctgtggttaaggggtgggaagaatatataaggtgggggtcttatgtag  
 4681 -----+-----+-----+-----+-----+-----+ 4740  
 tgtctagaaccgcacccaattcccaccctttcttatatattccacccccagaatacatc

BsiHKA I  
 Bsp1286I

ttttgtatctgttttgcagcagccgcgcgcgcctatgagcaccactcgtttgatggaagc  
 4741 -----+-----+-----+-----+-----+-----+ 4800  
 aaaacatagacaaaaactcgtcggcgggcggtactcgtggttgagcaaaactaccttcg

BstDSI  
 NcoI  
 StyI  
 BanII  
 BsiHKA I  
 Bsp1286I  
 SacI NspI  
 SphI BpmI

attgtgaggtcatatttgacaacgcgcgatgccccatgggcccgggtgcgtcagaatgtg  
 4801 -----+-----+-----+-----+-----+-----+ 4860  
 taacactcgagtataaaactgttgccgctacgggggtacccggccccacgcagttcttacac

Pfl1108I  
 BsaI  
 Bsp24I  
 BanII  
 Bsp1286I

atgggctccagcattgatggtcgccccgtcctgccccgaaactctactaccttgacctac  
 4861 -----+-----+-----+-----+-----+-----+ 4920  
 taccgcaggtcgtaactaccagcggggcaggacgggctttgagatgatggaactggatg

PstI  
 Eco57I  
 SfcI  
 Bsp24I  
 Bsp24I  
 EciI  
 Tth111I  
 Hin4I  
 MmeI SfcI  
 AlwNI  
 MspAII  
 PstI

gagacggtgtctggaacgcggttgagactgcagcctccgcccgttcagcgcgtgca  
 4921 -----+-----+-----+-----+-----+-----+ 4980  
 ctctggcacagaccttgccgcaacctctgacgtcggagggcgggcgaagtcggcgacgt

SacII  
 MspAII  
 BstDSI  
 BanII  
 Bsp1286I  
 Bpu10I  
 BstAPI  
 BtsI

gccaccgccccgggattgtgactgactttgtcttctgagcccgcttgcaagcagtgca  
 4981 -----+-----+-----+-----+-----+-----+ 5040  
 cgggtggcgggcgccctaactgactgaaacgaaaggactcgggcgaacgttcgtcacgt

BsgI

FIGURE 28

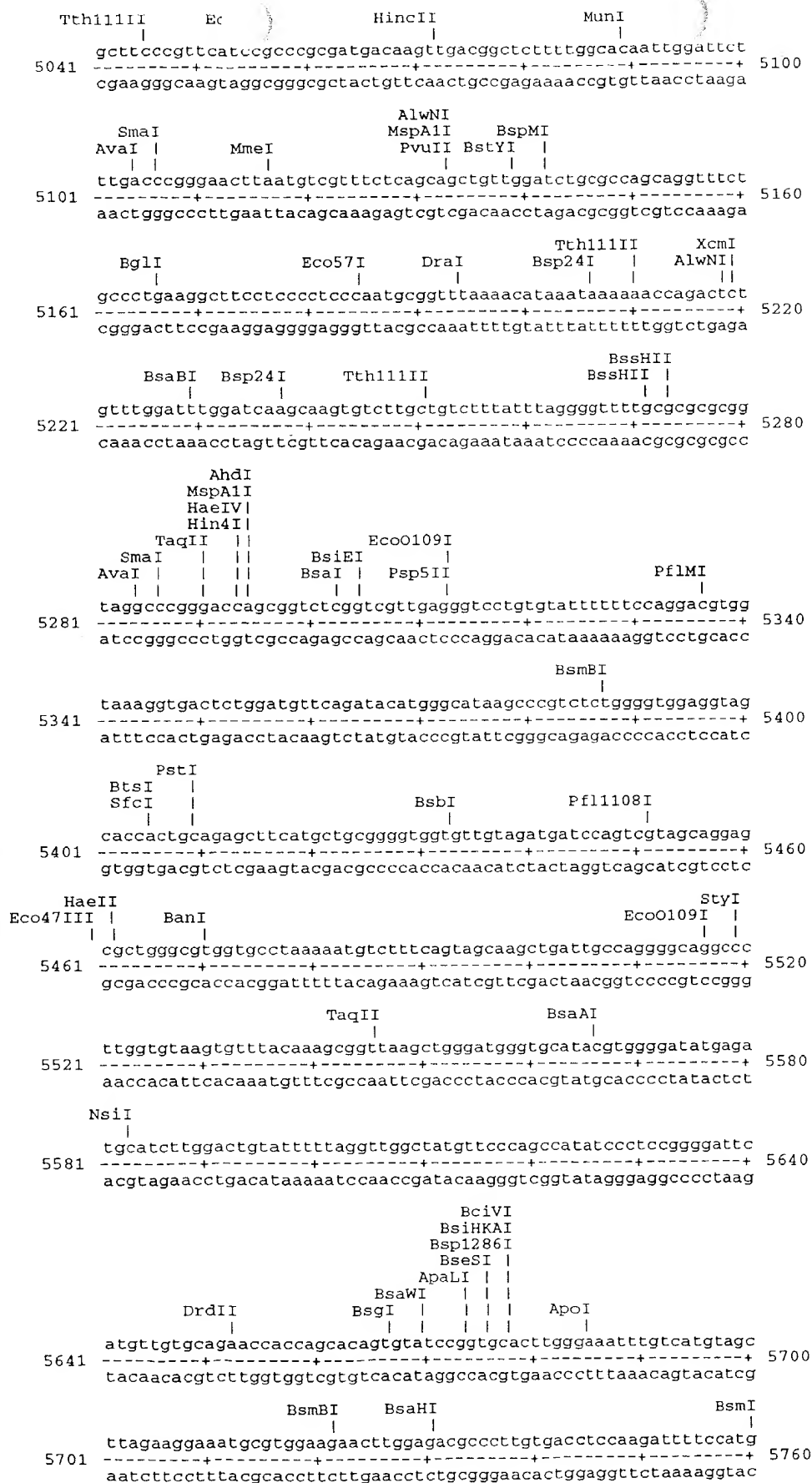


FIGURE 28

ApaI  
 BanII  
 Bsp1286I  
 BstDSI  
 BmgI  
 BseSI  
 BsrDI  
 BstXI  
 MslI  
 NsiI  
 5761  
 ctttcggtccataatgatggcaatgggcccacgggcggtgggcgaagatatcttg  
 gtaagcaggtattactaccgttacccgggtgcccgcgcgggacccgcttctataaagac  
 5820  
 MslI  
 HaeI  
 5821  
 ggatcactaacgtcatagtgtgttccaggatgagatcgatcaggccatttttacaag  
 octagtgttgaggtatcaacacaagggtcctactctagcagtatccggtaaaaaatgtttc  
 5880  
 EciI  
 BanI  
 DrdII  
 5881  
 cgccggcgagggtgccagactcggtataatggttccatccggccaggggcgtagtta  
 gcgcccgcctccacggtctgacgccatattaccaaggtaggccgggtcccgcgcatcaat  
 5940  
 AccI  
 5941  
 cctcacagatttgcatttccacgctttgagttcagatggggggatcatgtctacctgc  
 gggagtggtctaaacgtaaaagggtgcgaaactcaagtcacccccctagtagcagatggacg  
 6000  
 BspMI  
 MspAII  
 PvuII  
 6001  
 gggcgcatgaagaaaacggtttccggggtaggggagatcagctgggaagaaagcaggttc  
 ccccgctacttcttttgccaaaggccccctccctctagtcgaccttctttctgccaag  
 6060  
 ApaI  
 BanII  
 Bsp1286I  
 BmgI  
 BseSI  
 BspFI  
 HgiEIII  
 MspAII  
 PvuII  
 Bpu10I  
 6061  
 ctgagcagctgcgacttacgcagccggtgggcccgtaaatcacacctattaccgggtgc  
 gactcgctgacgctgaatggcgctcgccacccgggcatttagtggtgataatggcccacg  
 6120  
 MspAII  
 PvuII  
 PstI  
 AceIII  
 SfiI  
 Bpu10I  
 6121  
 aactggttagttaagagagctgcagctgcccgtcatccctgagcagggggccacttcgtta  
 ttgaccatcaattctctcgacgtcgacggcagtagggactcgccccccggtgaagcaat  
 6180  
 NspI  
 NspI  
 EciI  
 HaeII  
 6181  
 agcatgtccctgactcgcatgttttccctgaccaaactccgccagaaggcgctcgccgccc  
 tcgtacagggactgagcgtacaaaaggactggtttaggcggtcttccgcgagcggcggg  
 6240  
 BstAPI  
 BsaI  
 EciI  
 6241  
 agcgatagcagttcttgcaggaagcaaagtttttcaacggtttgagaccgtccgcgta  
 tcgctatcgtaagaacgttccttcgtttcaaaaagttgccaactctggcaggcgccat  
 6300  
 NspI  
 SphI  
 TaqII  
 Tth111III  
 RleAI  
 AceIII  
 BstEII  
 AarIII  
 6301  
 ggcatgctttttagcggtttgaccaagcagttccaggcggtcccacagctcggtcacctgc  
 ccgtacgaaaactcgcaaaactggttcgtcaaggtccgcccagggtgtcgagccagtggaacg  
 6360  
 BspMI  
 BseRI  
 6361  
 tctacggcatctcgatccagcatatctcctcggtttcgcggttggggcggttttcgctgt  
 agatgccgttagagctaggtcgatatagaggagcaaaagcgcccaaccccgccgaaagcgaca  
 6420  
 BspGI  
 BsiHKAI  
 Bsp1286I  
 BstDSI  
 BcgI  
 EcoO109I  
 Psp5II  
 6421  
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 6480

FIGURE 28



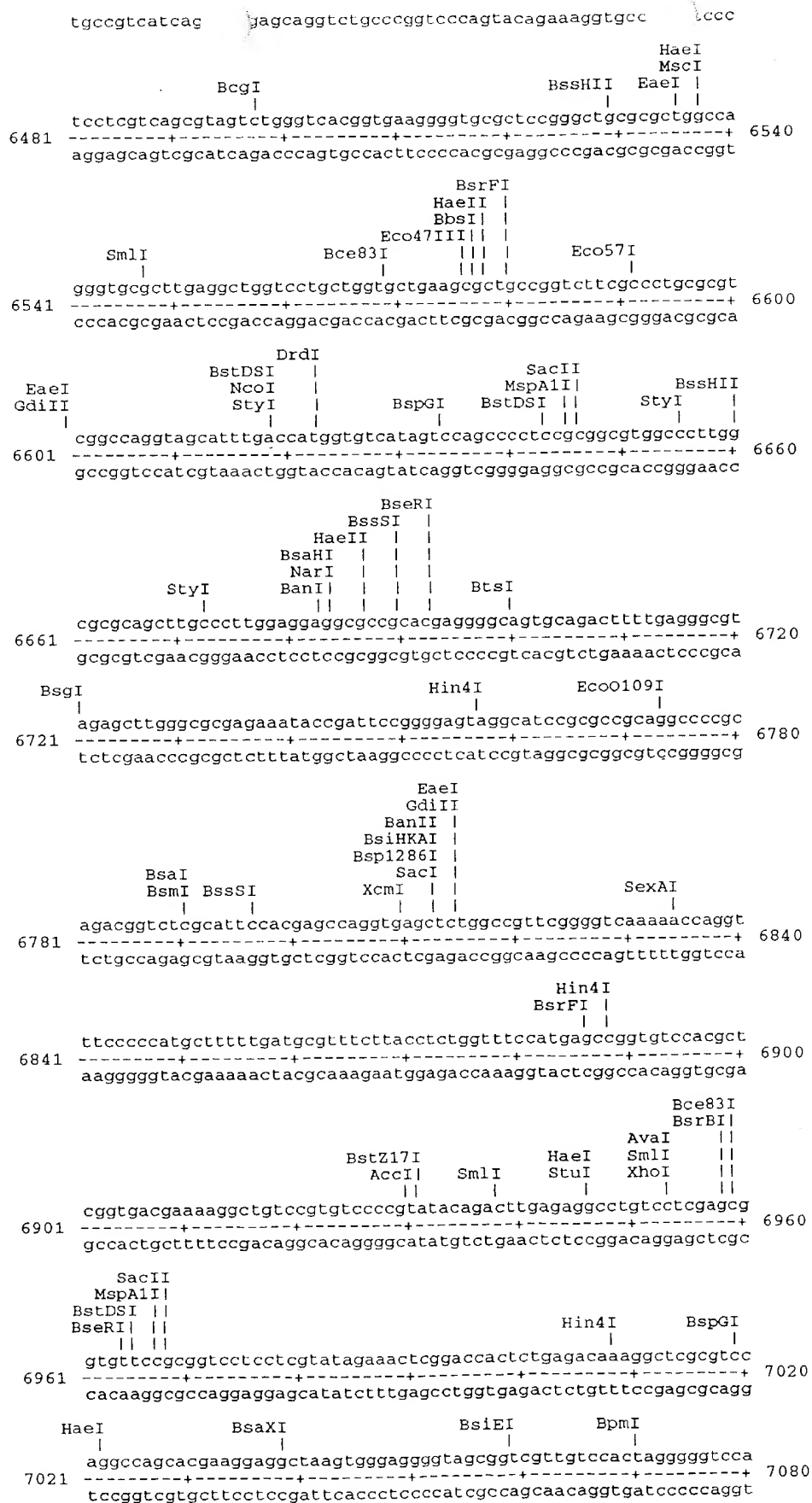


FIGURE 28

NspI  
 BbsI  
 PshAI  
 AflIII  
 BspLU111  
 EarI

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 gagcgagggtcccacacttctgtgtacagcgggagagccgtagttccttccactaaccaa

BsaAI  
 HaeI  
 PmlI  
 Eco57I

7141 tgtaggtgtaggccacgtgaccgggtgttctgaaggggggtataaaaggggtggggg 7200  
 acatccacatecgggtgactggccacaaaggacttcccccgatattttccccaccccc

EarI  
 PflMI  
 MspAII  
 PvuII  
 ScaI  
 TatI

7201 cgcgttcgtcctcactctcttcgcacgtgtgtctgcgaggccagctgttgggggtgagt 7260  
 gcgcaagcaggagtgcgagaaggcgtagcgacagacgctcccggtcgacaacccccactca

7261 actccctctgaaaagcgggcatgacttctgcgctaagattgtcagtttccaaaaacgagg 7320  
 tgagggagacttttcgcccgtactgaagacgcgattctaacagtcacagggtttttgctcc

BseRI  
 BstDSI  
 SacII  
 MspAII  
 EaeI  
 GdiII

7321 aggatttgatattcacctggcccgcggtgatgcctttgagggtggccgcatccatctggt 7380  
 tcttaactataagtggaccgggcccactacggaaactcccaccggcgtaggttagacca

HindIII  
 MmeI

7381 cagaaaagacaatctttttgtgtcaagcttggtggcaaacgaccgtagaggcggttg 7440  
 gtcttttctgttagaaaaacaacagttcgaaaccacggtttgctgggcatctcccgaacc

BssHII  
 BsiEI  
 PvuI  
 NruI  
 BsgI  
 EaeI  
 GdiII  
 StyI

7441 acagcaacttggcgatggagcgcagggtttggtttttgtcgcgatcggcgcgctccttgg 7500  
 tgcgttgaaccgctacctcggtcccaaaacacagcgtagccgcgcgaggaacc

BsaAI  
 BssHII

7501 ccgcgatgttttagctgcacgtattcgcgcgcaacgcacccgcatcgggaaagacggtgg 7560  
 ggcgctacaaatcgacgtgcataagcgcggttgctggtggcggttaagcccttctgccacc

BsiHKAII  
 Bsp1286I  
 BseSI  
 ApaLI  
 BstAPI  
 DraIII  
 Bsp1286I  
 SexAI  
 BmgI  
 BseSI  
 BanI  
 SacII  
 MspAII  
 BstDSI  
 HincII  
 Tth111I

7561 tgcgctcgtcgggaccaggtgcacgcgccaacccggttggtgcagggtgacaaggtcaa 7620  
 acgcgagcagcccgtggtccacgtgcgcggttggtgcgccaacacgtcccactgttccagtt

BsiEI  
 EaeI  
 EagI  
 GdiII  
 NotI

BsgI  
 HaeII  
 BspGI

7621 cgctgggtggctacctctccgcgtaggcgctcgttggtccagcagaggcggccgccttgc 7680  
 gcgaccaccgatggagaggcgcatccgcgagcaaccaggtcgtctccgcggcggggaacg

BsmBI  
 BstDSI

7681 gcgagcagaatggcggtaggggtctagctgcgtctcgtccgggggtctgcgtccacgg 7740  
 cgtcgtcttaccgccatccccagatcgacgcagagcaggccccccagacgcaggtgcc

FIGURE 28

SmaI  
 Aval | BssHII  
 7741 taaagaccccgggcagcagcgcgcgctcgaagtagtctatcttgcatccttgcaagtcta 7800  
 atttctggggccgctcgctccgcgcgagcttcatcagatagaacgtaggaacgttcagat  
 BstDSI  
 EcoO109I |  
 Psp5II NcoI  
 HaeII BssHII BssHII | SanDI StyI  
 7801 gcgctctgctgcatgcgcgggcggaagcgcgcgctcgatgggttgagtgggggacccc 7860  
 cgcgagcgagcgtacgcccccgcttcgcgcgagcagcaccactcaccctcgggg  
 PflMI  
 TaqII | NspI | Hin4I  
 7861 atggcatgggggtgggtgagcgcgaggcggtacatgccgcaaatgtcgtaaacgtagaggg 7920  
 taccgtacccacccactcgcgccctcgcatgtacggcgtttacagcatttgcatctccc  
 SacII  
 MspAII |  
 BstDSI | BssHII |  
 BanII Bsp1286I BpII |  
 7921 gctctctgagtagttccaagatatgtagggttagcatcttccaccgaggatgctggcgcgca 7980  
 cgagagactcataaggttctatacatcccatcgtagaaggtggcgccctacgaccgcggt  
 BsaAI | BseRI | TaqII |  
 7981 cgtaatcgtagtctcgtagcgaggagcgaggaggtcgggaccgaggttgctacggggcg 8040  
 gcattagcatatcaagcacgctccctcgctcctccagccctgggtccaacgatgcccgcc  
 MmeI NspI  
 BbsI | MmeI | Eco57I |  
 8041 gctgctctgctcggaagactatctgcctgaagatggcatgtgagttggatgatatggttg 8100  
 cgacgagacgagccttctgatagacggaacttctaccgtacactcaacctactataccaac  
 BsaI  
 BbsI BsaHI |  
 8101 gacgctggaagacgttgaagctggcgctctgtgagacctaccgctcacgcacgaaggagg 8160  
 ctgcgaccttctgcaacttcgaccgcagacactctggatggcgagtgctgcttccctcc  
 BsgI AceIII BspMI  
 HincII | BstEII | DrdI |  
 8161 cgtaggagtcgcgagcttgttgaccagctcgcggtgacctgcacgtctagggcgagtg 8220  
 gcacccctcagcgctcgaaacaactggtcgagccgccaactggacgtgcagatcccgcgctca  
 BspGI  
 8221 agtccaggggttcccttgatgatgtcatacttatectgtccctttttttccacagctcgc 8280  
 tcaggtcccaaggaactactacagtatgaataggacagggaaaaaaagggtgtcgagcg  
 ScaI  
 AceIII | EarI | TatI |  
 8281 ggttgaggacaaactcttcgcggtctttccagtagctcttgatcggaaccgctcggcct 8340  
 ccaactcctggttgagaagcgccagaagggtcatgagaacctagcctttgggcagccgga  
 NspI HincII BglI  
 8341 ccgaacggtaagagcctagcatgtagaactggttgacggcctggtaggcgcagcatccct 8400  
 ggcttgccattctcgatcgtagatcttgaccaactgcggaccatccgcgtcgtaggga  
 TaqII  
 RleAI |  
 BsaWI |  
 BglI BspEI |  
 8401 tttctacgggtagcgcgctatgctcgcgcccttcgggagcgaggtgtgggtgagcgcaa 8460  
 aaagatgcccatcgcgcatagcgagcgccggaaggcctcgctccacacccactcgcggt  
 EciI  
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FIGURE 28





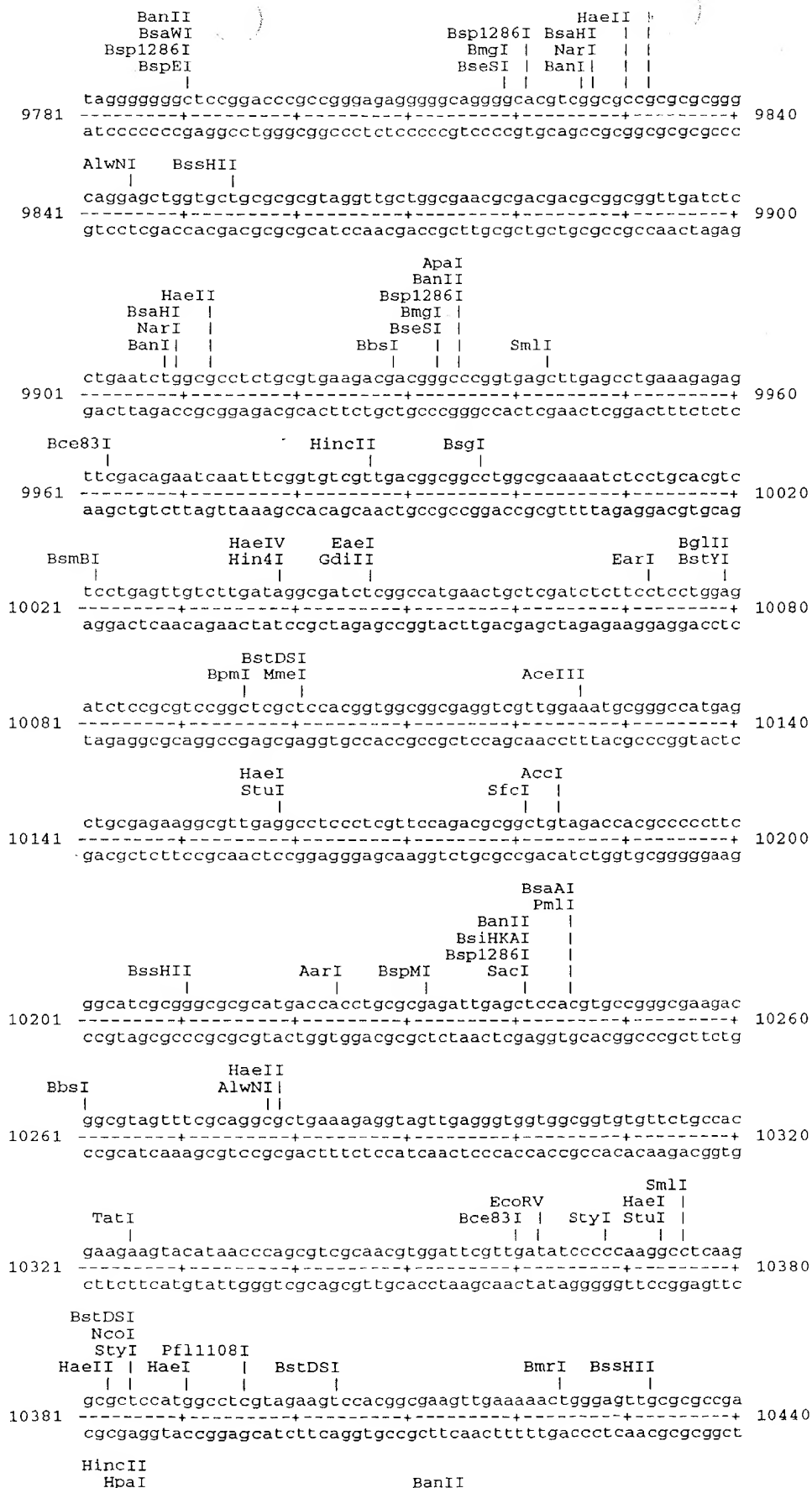


FIGURE 28

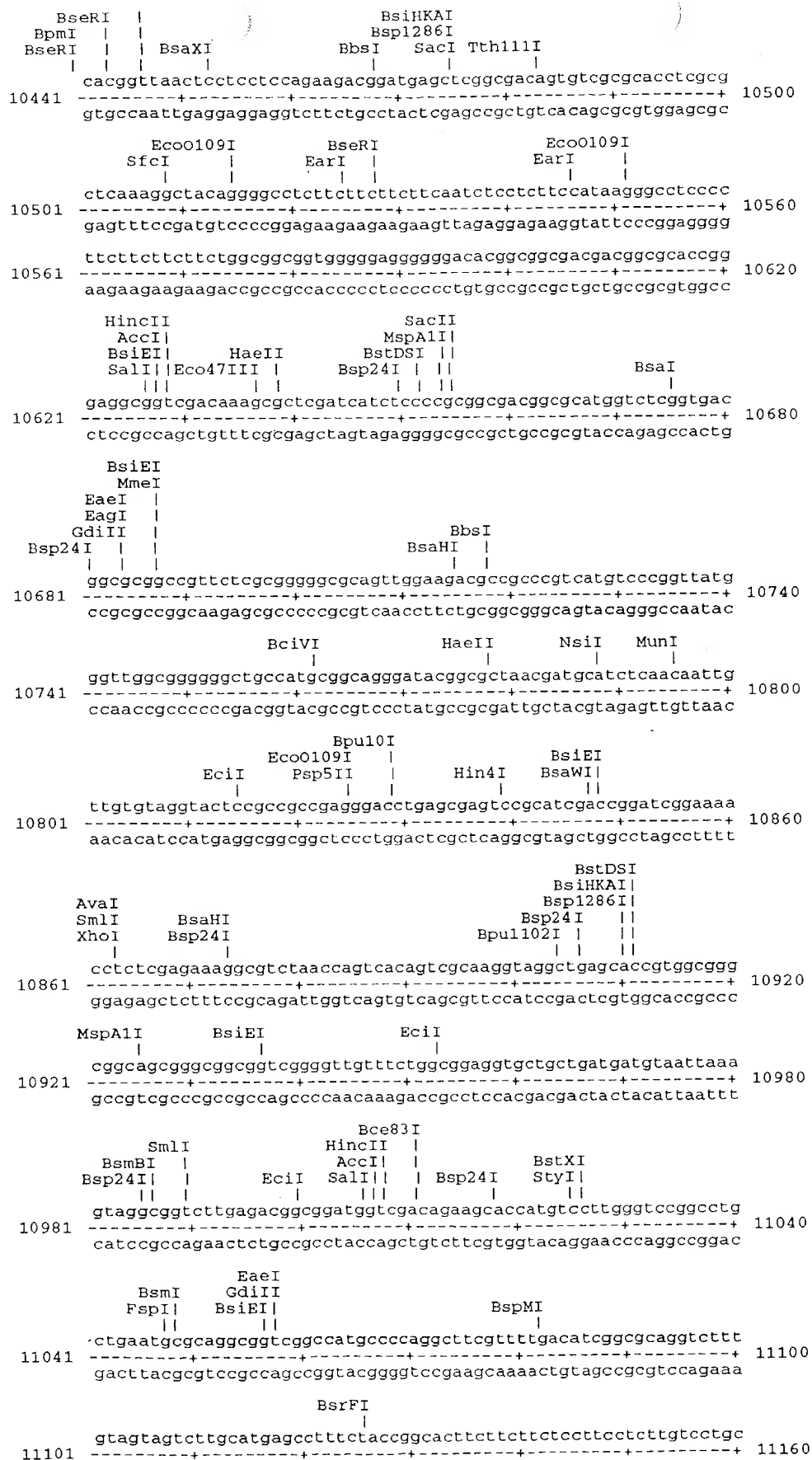


FIGURE 28

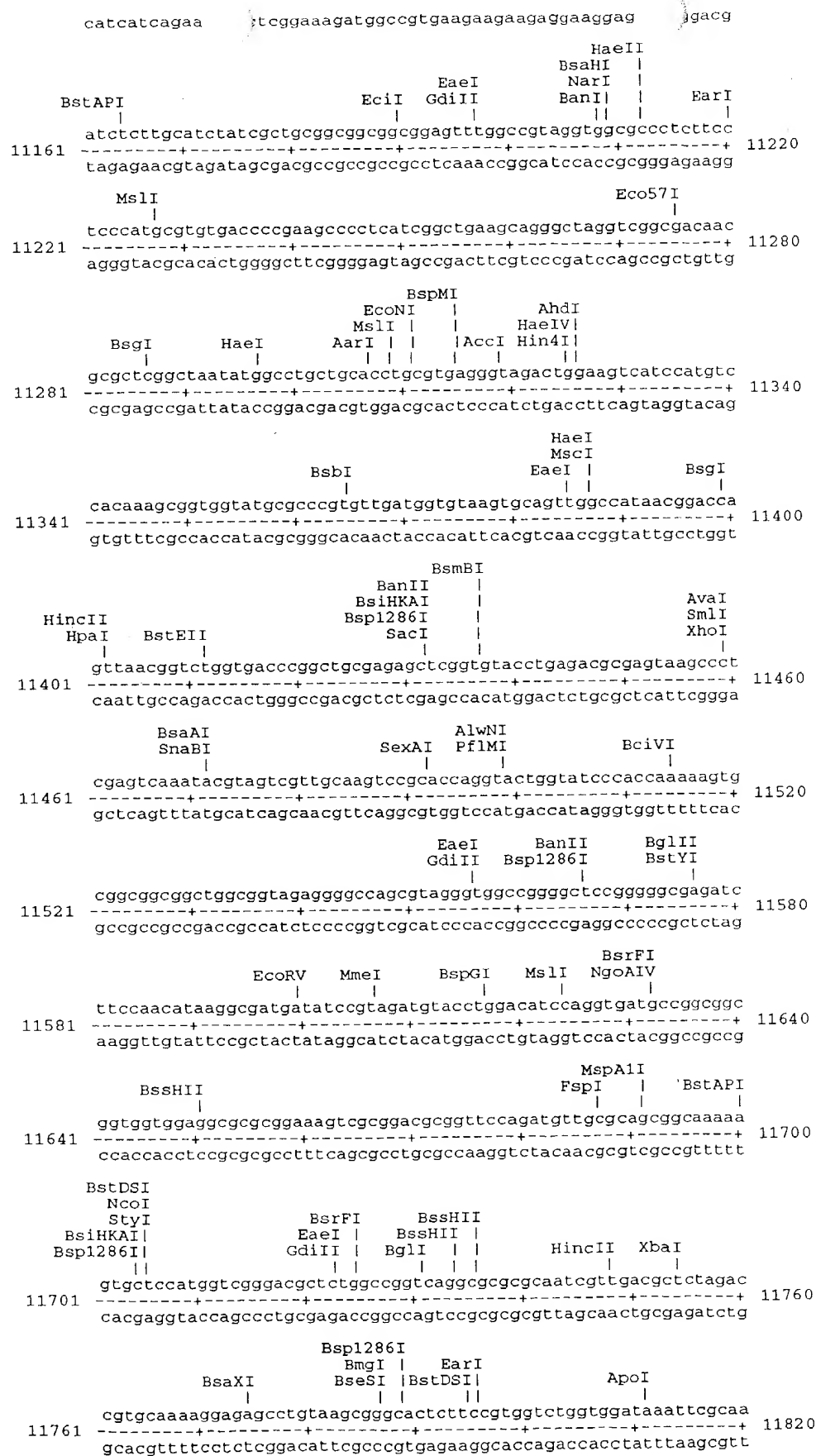


FIGURE 28



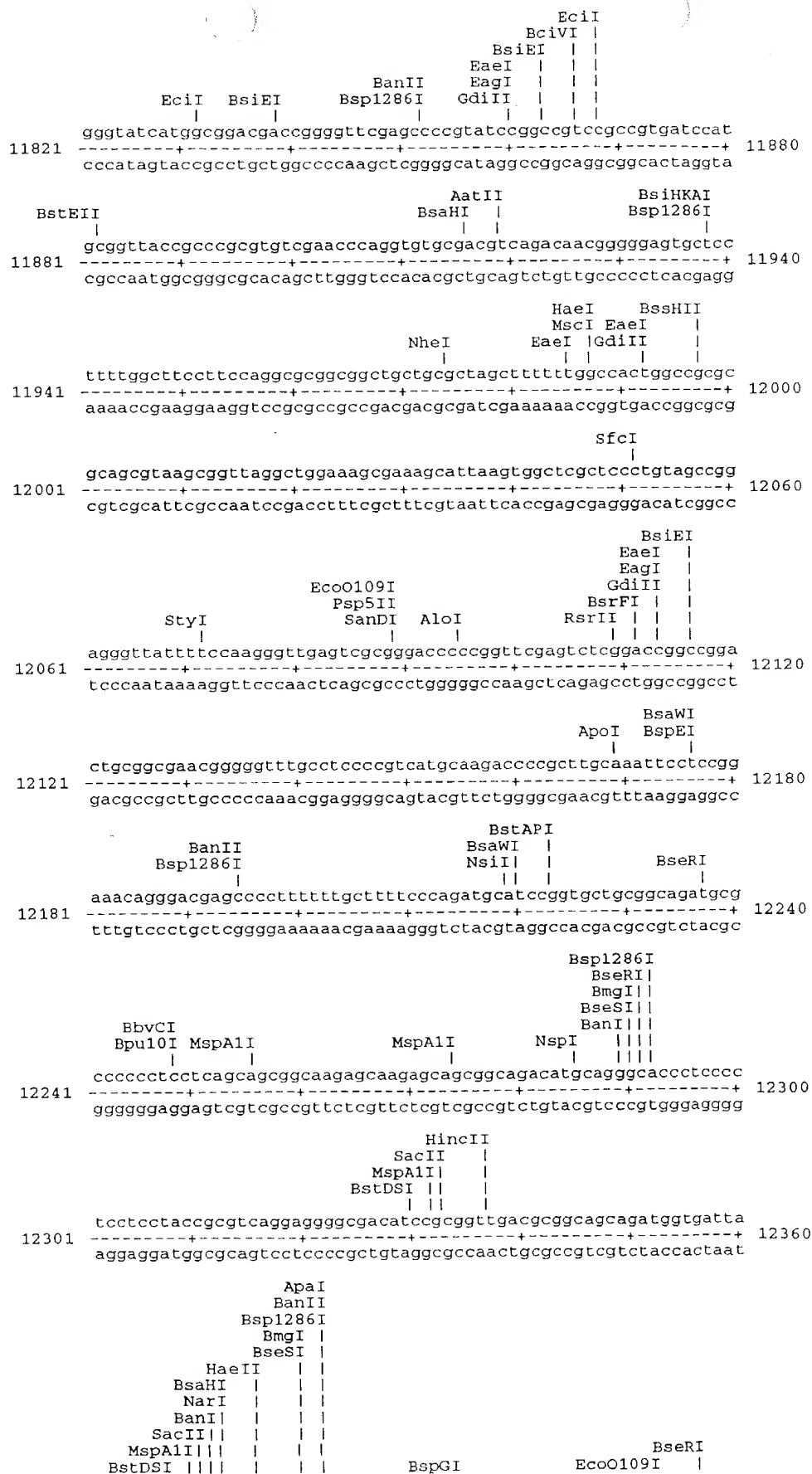


FIGURE 28

12361 cgaacccccgcg\_ ccgggcccgcactacctggacttgaggaggcgag\_ actggc 12420  
 gcttggggggcgccgcggcccgccgctgatggacctgaacctcctcccgctcccggaaccg

BanI BsrBI StyI MspAII BsgI  
 HaeII Bpu10I KpnI PvuII AflIII MluI  
 12421 gcggttaggagcgccctctcctgagcgggtacccaagggtgcagctgaagcgtgatacgcg 12480  
 cgccgatcctcgcgggagaggactcgccatgggttcccacgtcgacttcgcactatgcgc

SacII MspAII BstDSI  
 BsaAI SunI AlwNI NruI BsiEI BanII Bsp1286I  
 Eco57I AvaI  
 12481 tgaggcgtagctgcccgcgcagaaacctgttccgcgacgcgagggagaggagcccagga 12540  
 actccgcatgcacggcgccgtcttggacaaagcgtggcgctccctctcctcgggctcct

HaeIV Hin4I AhoI BseRI BsrBI  
 BseRI BseRI AceIII HaeI NruI  
 12541 gatcgccggatcgaaagtccacgcagggcgagctgcggcatggcctgaatcgcgagcg 12600  
 ctacgccttagctttcaagtgctcccgctcgacgccgtaccggacttagcgctcgc

BanII Bsp1286I BssHII  
 BseRI BssHII  
 12601 gttgctgcgcgaggaggactttgagcccgacgcgcgaaccgggattagtcgcgcgcgcg 12660  
 caacgacgcgctcctcctgaaactcgggctgcgcgcttggccctaatacaggcgcgcgcg

BsiEI EaeI EaeI GdiII  
 BsaAI PmlI BstEII DrdII  
 AflIII NotI SexAI  
 12661 acacgtggcgccgcgcgacctggtaaccgcatacagcagacgggtgaaccaggagattaa 12720  
 tgtgcaccgcgcggcggtggaccattggcgctatgctcgtctgccacttggctcctctaatt

SunI BsaAI PmlI BssHII SfcI  
 HindIII  
 12721 ctttcaaaaaagctttaacaaccagtgctacgcttgtggcgcgagggaggtggctat 12780  
 gaaagttttttcgaaattgttgggtgcacgcacgcgaacaccgcgcgctcctccaccgata

RleAI BseRI NsiI BssHII BpmI  
 12781 aggactgatgcatctgtgggactttgtaagcgcgctggagcaaaacccaaatagcaagcc 12840  
 tcctgactacgtagacaccctgaaacattcgcgcgacctcgttttgggtttatcggtcgg

BsrBI MspAII PvuII BsmI BsgI  
 12841 gctcatggcgagctgttccttatagtgacagcacagcagggacaacgaggcattcagga 12900  
 cgagtaccgcgctgcacaaggaatatcacgtcgtgctcctcgttgctccgtaagtcct

BanII Bsp1286I AvaI MspAII BsaBI SfcI  
 12901 tgcgctgctaaacatagtagagcccagggcccgctggctgctcgatttgataaacatcct 12960  
 acgcgacgatttgtatcatctcgggctcccggcgaccgacgagctaaactattttagga

PstI MslI SmlI BsgI Bce83I EaeI GdiII  
 12961 gcagagcatagtggtgcaggagcgagcttgagcctggctgacaaggtggccgcatcaa 13020  
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FIGURE 28

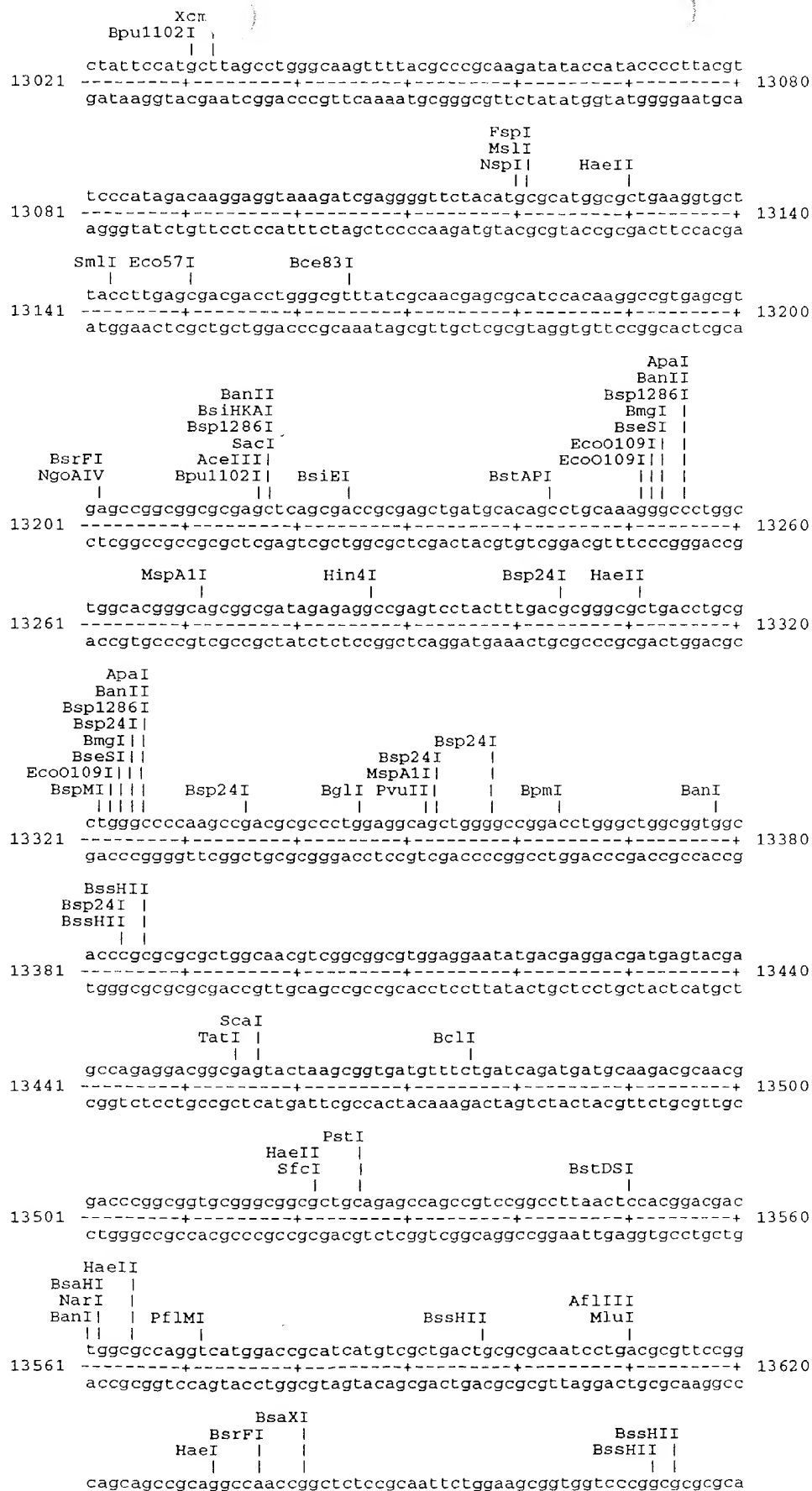


FIGURE 28



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BstYI DraI BseRI BseRI BsaAI  
 | | | | |  
 14401 aagatccccctcggtgcacagtttaaacagcgaggaggagcgcatTTTgcgctacgtgcag 14460  
 ttctaggggagcaacgtgtcaaatTTTgcgctcctcctcgcgtaaaacgcatgcacgtc

BspGI HaeII XcmI  
 | | |  
 14461 cagagcgtgagccttaacctgatgcgcgacgggtaacgcccagcgtggcgctggacatg 14520  
 gtctcgactcggaaattggactacgcgctgccccattgcgggtcgaccgacgtgtac

BsiEI EaeI EagI GdiIII BsrFI  
 | | | | |  
 14521 accgcgcgcaacatggaaccgggcatgtatgcctcaaaccggccgtttatcaaccgccta 14580  
 tggcgcgctgttaccttggcccgtaacacggagtttggccggcaaatagttggcggt

BsiEI EaeI EagI GdiIII NotI AvaI  
 | | | | |  
 14581 atggactacttgcacgcgcggccgctgaaccccgagtatttcaccaatgccatcttg 14640  
 tacctgatgaacgtagcgcgcggcgccacttggggctcataaagtggttacggtagaac

Bsp1286I AvaI BmgI BseSI BanI  
 | | | | |  
 14641 aaccgcgactggctaccgccccctggtttctacacgggggattcgaggtgcccaggggt 14700  
 ttggcgctgaccgatggcgggggaccaaagatgtggccccctaagctccacgggctcca

AlwNI BstAPI  
 | |  
 14701 aacgatggattcctctgggacgacatagacgacgctgttttccccgcaaccgcagacc 14760  
 ttgctacctaaggagaccctgctgtatctgctgtgcacaaaagggcgcttggcgctctgg

HaeII HindIII  
 | |  
 14761 ctgctagagtTgcaacagcgcgagcaggcagaggcgcgctgcgaaaggaaagcttccgc 14820  
 gacgatctcaacgttTgcgcgctcgtctcgcgcgcgacgcttctcttcgaaggcg

SacII MspAII BstDSI  
 | | |  
 14821 agggcaagcagcttTgctcgatctaggcgctgcggcccccggtcagatgctagtagccca 14880  
 tccggttcgtcgaaacaggctagatccgcgacggggcgccagctacgatcatcggt

HindIII Hin4I BsaI BglI  
 | | | |  
 14881 tttccaagcttgatagggtctcttaccagcactcgccaccaccgcccgcgctgctgggc 14940  
 aaaggttcgaactatcccagagaatggctcgtgagcgtggtggggcgcgcgacgacccg

BseRI BseRI SfcI PstI BspMI  
 | | | | |  
 14941 gaggaggagtacctaacaactcgctgctgcagcgcgagcgcgaaaaaacctgcctccg 15000  
 ctctcctcatggattTgttgagcgacgacgtcggcgtcgcgctttttttggacggaggc

BbsI SunI  
 | |  
 15001 gcatttcccaacaacgggatagagagcctagtggacaagatgagtagatggaagacgtac 15060  
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FIGURE 28

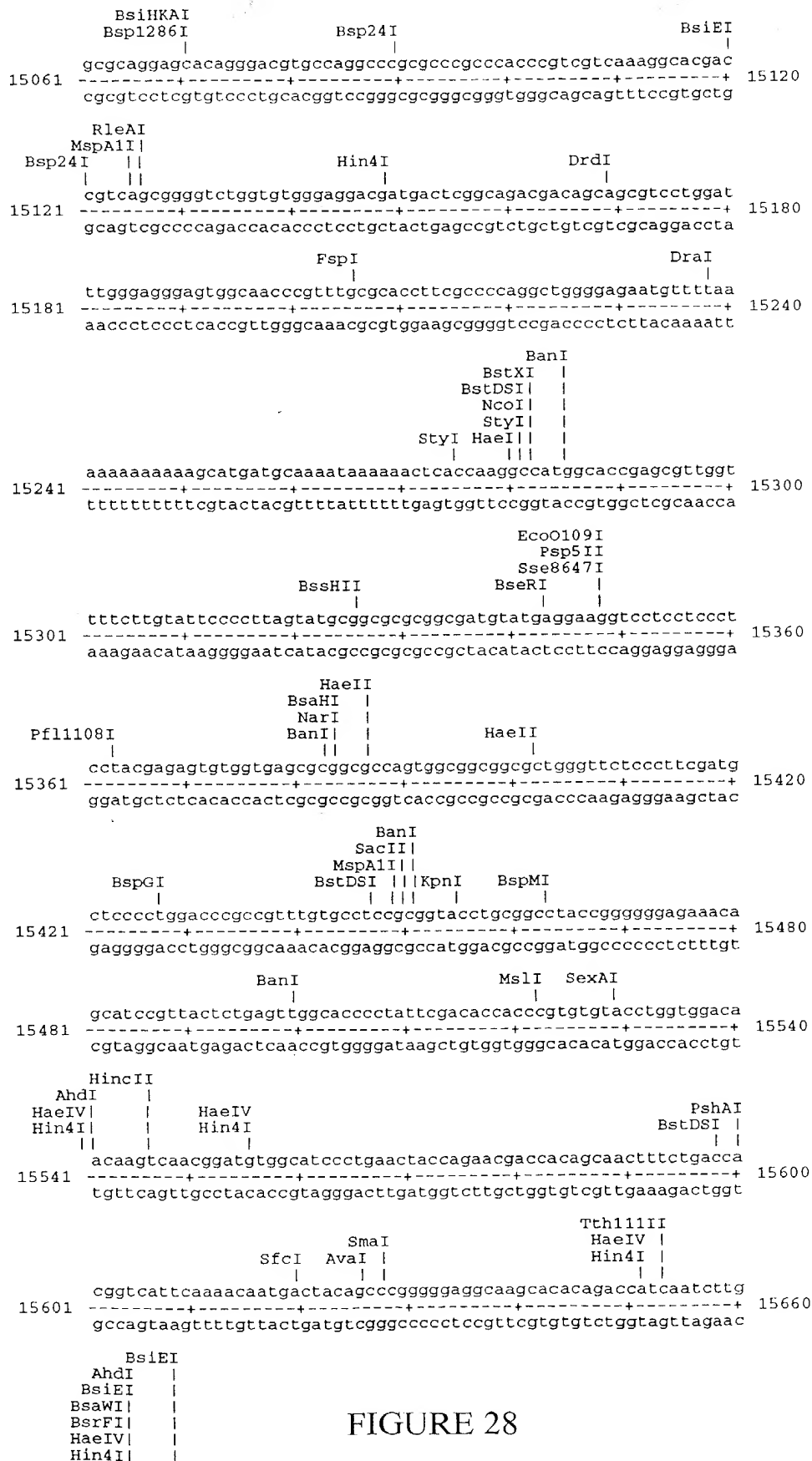


FIGURE 28



PinAI BclI EcoNI

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 tcttctttggccactagtttggggactgtctcctgtcgttctttgcgtcaatgttggatt

BanI  
 TaqIII  
 MspAII  
 PvuII

BsrDI BmrI HgiEII KpnI

16501 taagcaatgacagcaccttcacccagtaccgcagctgggtaccttgcatataactacggcg 16560  
 attcgttactgtcgtggaagtgggtcatggcgctgaccatggaacgtatgttgatgccgc

BsaWI BsrBI BspMI

16561 accctcagaccggaatccgctcatggaccctgctttgactcctgacgtaacctgcggct 16620  
 tgggagtctggccttaggcgagtacctgggacgaaacgtgaggactgcattggacgcgca

AccI BsrBI

16621 cggagcaggtctactggctgttgcagacatgatgcaagaccccgtagccttcgctcca 16680  
 gcctcgtccagatgaccagcaacggtctgtactacgttctggggcactggaaggcgaggt

HaeII BsiHKAI  
 BsaHI Bsp1286I  
 AceIII NarI BseSI  
 BsaWI BanI ApaLI

16681 cgcgccagatcagcaactttccggtgggtggcgccgagctgttgcctgcactccaaga 16740  
 gcgcgggtctagtcgttgaaaggccaccacccggtctgacaacgggcacgtgaggttct

AccI EciI

16741 gcttctacaacgaccaggcgttctactcccaactcatccgacagtttacctctctgaccc 16800  
 cgaagatgttgctggtccggcagatgaggttgagtagggcgtcaaatggagagactggg

BsaAI PmlI AscI  
 AflIII BssHII  
 AvaI DrdII PflMI

16801 acgtgttcaatcgctttcccgagaaccagattttggcgccgcccagccccaccatca 16860  
 tgcaacagttagcgaaagggtctcttggtctaaaaccgcgcggcggtcgggggtggtagt

AclI XmnI MspAII BcgI FspI

16861 ccaccgtcagtgaaaacgttctctgtctcacagatcacgggacgctaccgctgcgcaaca 16920  
 ggtggcagtcacttttgcaaggacgagagtgctagtgcctgcatggcgacgcgttgt

BseRI BcgI BsaHI BsaHI AarI BspMI

16921 gcatcgaggaggtccagcgagtgaccattactgacgccagacgcgcacctgcccctacg 16980  
 cgtagcctcctcaggtcgctcactggtaatactgactgcggtctgcggcgtggacggggatgc

EcoO109I

16981 tttacaaggccctgggcatagtctcgcgcgctcctatcgagccgcactttttgagcaa 17040  
 aaatgttccgggaccggtatcagagcggcgcgaggatagctcggcgtgaaaaactcgtt

NspI Tth111II EcoO109I Tth111II

17041 gcatgtccatccttatatcgcccagcaataacacaggtctggggcctgcgcttcccaagca 17100  
 cgtacaggttaggaatatagcgggtcgttattgtgtccgaccccgacgcgaagggttcgt

Bsp1286I BmgI BseSI  
 HaeII DraIII MmeI  
 Tth111II Eco47III BsbI BmrI TaqII

17101 agatgtttggcgggccaagaagcgctccgaccaacacccagtgcgctgcgcgggcact 17160  
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FIGURE 28



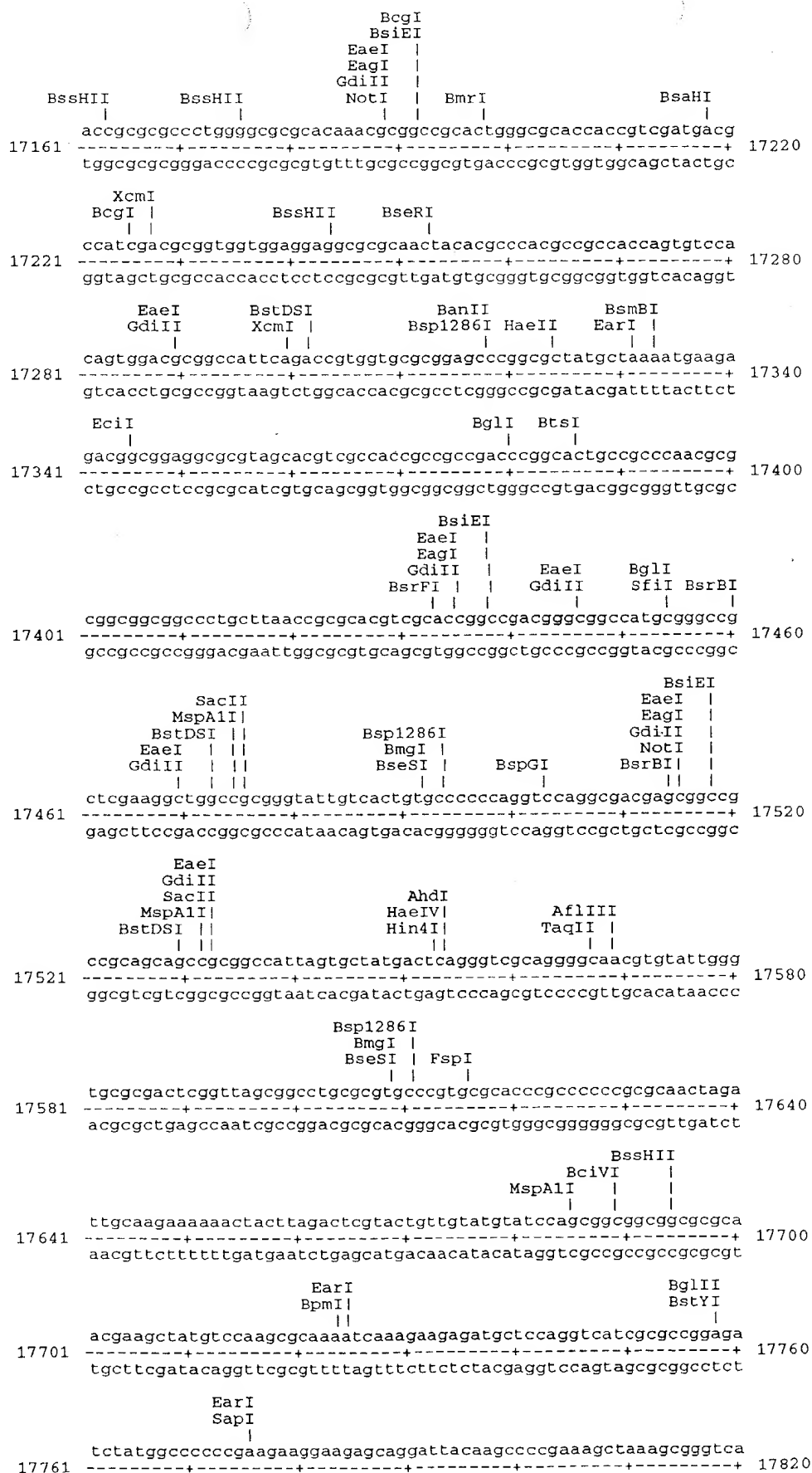


FIGURE 28



DrdI                    B                    EciI                    BsiEI  
 |                    |                    |                    |  
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 -----+-----+-----+-----+-----+-----+-----+-----+  
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 BstDSI  
 |  
 18481 cgtccaagacctctacggaggtgcaaacggaccgctggatgtttcgcggtttcagccccc 18540  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 gcaggttctggagatgcctccacgtttgcctgggcacctacaaagcgcaaagtcgggggg  
  
 HaeII                    HaeII  
 BsaHI                    BsaHI  
 NarI                    NarI  
 BanI                    BanI                    BssHII  
 |                    |                    |                    |  
 18541 ggcgcccgcgcggttcgaggaagtacggcgccgcagcgcgctactgcccgaatatgcc 18600  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 ccgcgggcgcgccaagctccttcatgcccgggcggtcgcgcgatgacgggcttatacggg  
  
 BsrDI  
 |  
 18601 tacatccttccattgcgccctaccccggtatcggtggctacacctaccgccccagaagac 18660  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 atgtaggaaggtaacgcggatgggggcccgatagcaccgatgtggatggcggggtcttctg  
  
 BbsI                    BsaHI                    DrdII  
 |                    |                    |  
 18661 gagcaactaccgacgcccgaaccaccactggaaccgcgcgcgcgtcgccgctgccagc 18720  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 ctcggtgatgggtcgcggttggtgggtgacctggggcgcgcgccagcgccagcggtcg  
  
 BcgI                    FspI                    NruI                    EcoO109I  
 |                    |                    |                    |  
 18721 ccgtgctggccccgatttccgtgcgcagggtggctcgcggaaggaggcaggaccctgggtgc 18780  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 ggcacgaccggggctaaaggcacgcgtcccaccgagcgcttctcctcgctctgggaccacg  
  
 BssHII                    BsrFI                    DraI                    DrdII  
 |                    |                    |                    |  
 18781 tgccaacagcgcgctaccaccccagcatcggtttaaagccggtctttgtggttcttgcag 18840  
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 acggttgctgcgcgatggtggggtcgtagcaaatcttcggccagaaacaccaagaacgtc  
  
 AarI                    BspMI                    BanI                    BsmI  
 |                    |                    |                    |  
 18841 atatggccctcacctgcccctcgttttcccggtgccgggattccgaggaagaatgcacc 18900  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 tataccgggagtggaaggcgaggcaagggccacggccctaaggctccttcttacgtgg  
  
 BstDSI  
 FseI  
 EaeI  
 GdiII  
 BsrFI  
 NgoAIV  
 EaeI  
 GdiII  
 BglI                    NspI                    SphI                    FspI                    BsrFI  
 |                    |                    |                    |                    |  
 18901 gtaggaggggcatggcgccacggcctgacggcgggcatgcgtcgctgcgcaccaccggc 18960  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 caccctcccgtaccggccggtgcgggactgcccgcgtacgcagcacgcgtggtggcgg  
  
 BssHII                    NspI                    SphI                    BciVI  
 |                    |                    |                    |  
 18961 ggccgcgcgcgctgcaccgtgcgatgcgcggcggtatcctgccctccttattocactga 19020  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 ccgccgcgcgagcgtggcagcgtacgcgcgccataggacggggaggaataaggtgact  
  
 Bsp1286I  
 BmgI  
 BseSI  
 HaeII  
 SacII                    BsaHI  
 MspAII                    NarI  
 BstDSI                    BanI  
 |                    |                    |                    |  
 19021 tcgccgcgcgcatggcgccgtgcccgaattgcacgtcggttccttgaggcgagagac 19080  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 agcgggcgcgctaaccggcgacgggccttaacgtaggcacgggaacgtccgcgtctctg  
  
 NspI                    BspGI  
 |                    |  
 19081 actgattaaaaacaagttgcatgtggaataaataaaagtctggactctcacgct 19140  
 -----+-----+-----+-----+-----+-----+-----+-----+  
 tgactaattttgttcaacgtacaccttttagttttttttttcagacctgagagtgcca

FIGURE 28



FIGURE 28

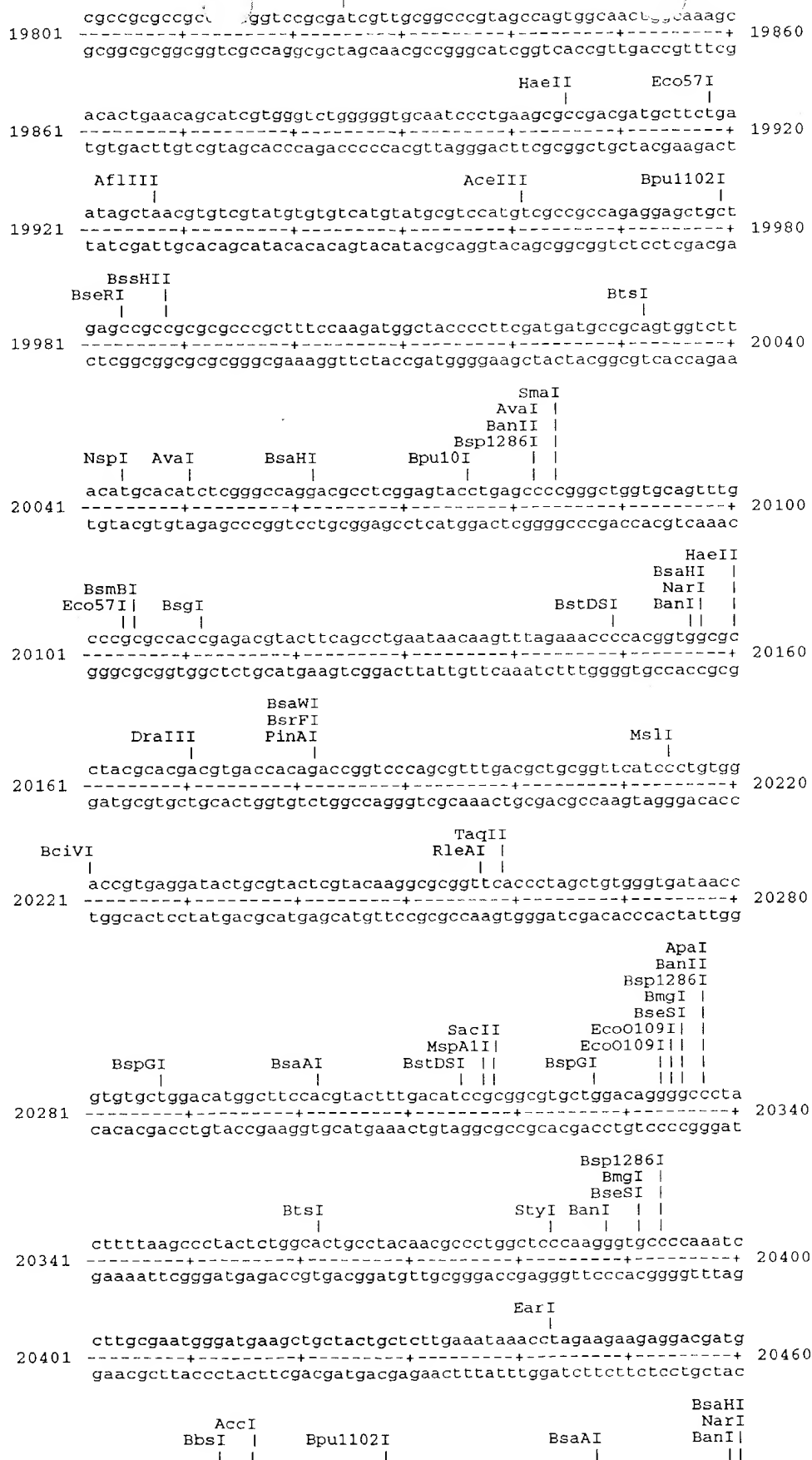


FIGURE 28

20461 acaacgaagac agacgagcaagctgagcagcaaaaaactcacgtat gcagg 20520  
 tgttgcttctgcttcctcgtcgttcgactcgtctttttgagtgacataaacccgtcc

HaeII SspI  
 20521 cgccttattctggtataaatattacaaaggagggtattcaaatagggtgcgaagggtcaaa 20580  
 gcggaataagaccatatttataatgtttctctccataagtttatccacagcttccagttt

Tth111II EcoNI  
 20581 cacctaaatatgccgataaaacatttcaacctgaacctcaaataggagaatctcagtggt 20640  
 gtggatttatacggctattttgtaaagttggacttggagtttatcctcttagagtcacca

VspI MspAII PvuII  
 20641 acgaaactgaaattaatcatgcagctgggagagtccttaaaaagactaccccaatgaaac 20700  
 tgctttgactttaattagtagctcgacctctcaggaattttctgatggggttactttg

NdeI RleAI BsmI  
 20701 catgttacggttcatatgcaaaacccacaaatgaaatggagggaaggcattcttgttaa 20760  
 gtacaatgccaaagtatacgttttgggtgtttacttttacctccgttccgtaagaacatt

20761 agcaacaaaatggaaagctagaaagtcagtggaatgcaatttttctcaactactgagg 20820  
 tcgttggttttacctttcgatctttcagttcacctttacgttataaaagagttgatgactcc

BsiEI BsrDI BsrGI TatI  
 20821 cgaccgcaggcaatggtgataacttgactcctaaagtgtattgtacagtgaagatgtag 20880  
 gctggcgctcgttaccactattgaactgaggatttcaccataacatgtcacttctacatc

NspI BssSI  
 20881 atatagaaacccagacactcatattttcttacatgcccactattaaggaaggtaactcac 20940  
 tatatctttggggtctgtgagtataaagaatgtacgggtgataattccttccattgagtg

HaeI StuI BglI BsrDI  
 20941 gagaactaatgggccaacaatctatgcccaacaggcctaattacattgcttttagggaca 21000  
 ctcttgattaccgggtgttagatagcggttggtcgggattaatgtaacgaaaatccctgt

TaqII  
 21001 attttatttggtctaatgtattacaacagcacgggtaatatgggtgttctggcgggccaag 21060  
 taaaataaccagattacataatgttgctggtgccattatacccacaagaccgcccgttc

Tth111II BsmI Tth111II  
 21061 catcgagttgaatgctgtttagatttgcaagacagaaacacagagctttcataccagc 21120  
 gttagcgtcaacttacgacaacatctaaacgttctgtctttgtgtctcgaaagtatggtcg

DrdII SexAI HincII  
 21121 ttttgcttgattccattggtgatagaaccagggtacttttctatgtggaatcagggtgttg 21180  
 aaaacgaactaaggttaaccactatcttggtccatgaaaagatacaccttagtccgacaac

21181 acagctatgatccagatgttagaattattgaaaatcatggaactgaagatgaacttccaa 21240  
 tgtagactaggtctacaatcttaataacttttagtaccttgacttctactgaaggtt

Eco57I BmrI VspI StyI  
 21241 attactgctttccactgggaggtgtgattaatacagagactcttaccagggtaaaacctta 21300  
 taatgacgaaagggtgacctccacactaattatgtctctgagaatggttccattttggat

EcoNI SfcI ApoI MmeI  
 21301 aaacagggtcaggaaaatggatgggaaaaagatgtacagaattttcagataaaaatgaaa 21360  
 tttgtccagtccttttacctacctttttctacgatgtcttaaaagtctatttttacttt

FIGURE 28

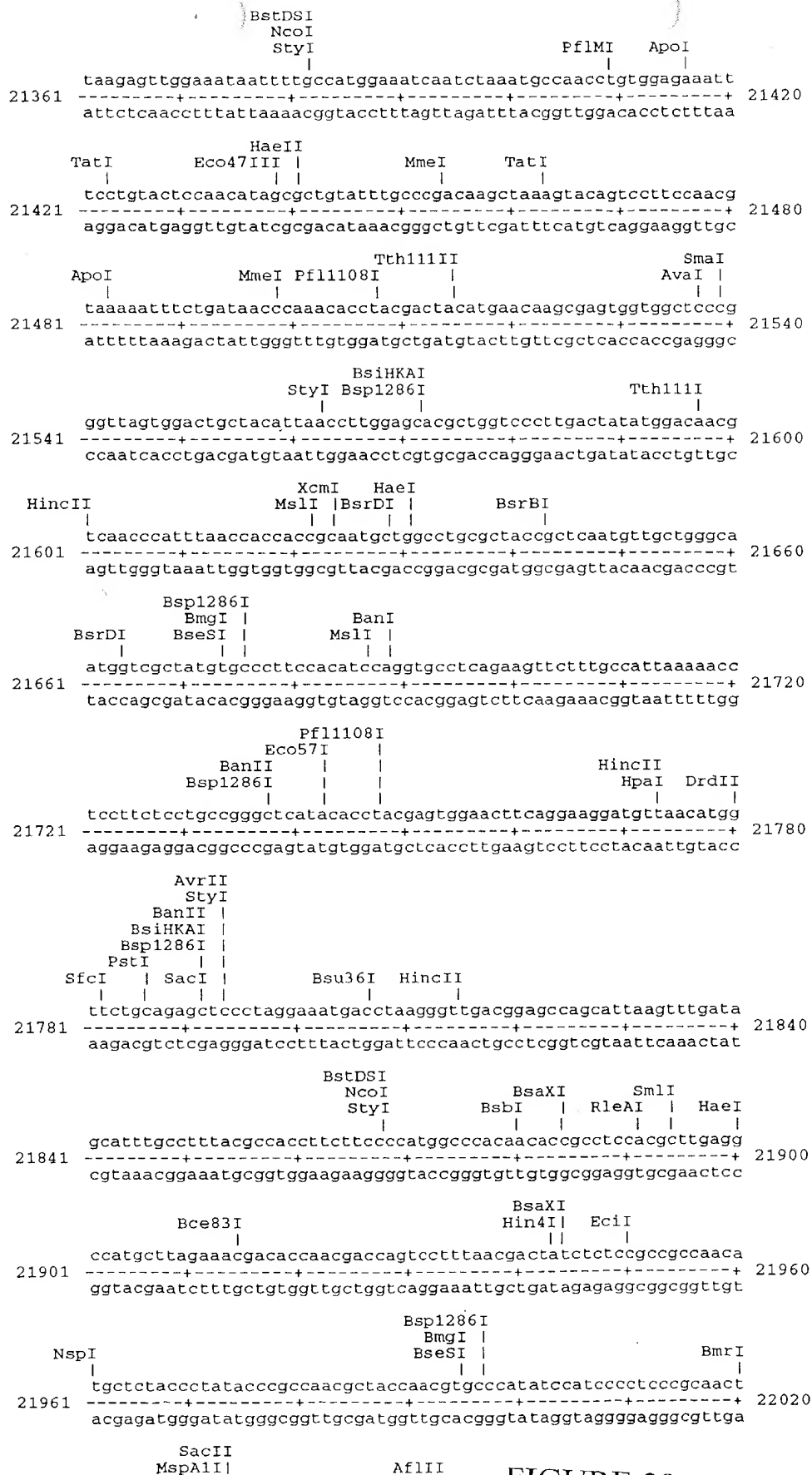


FIGURE 28





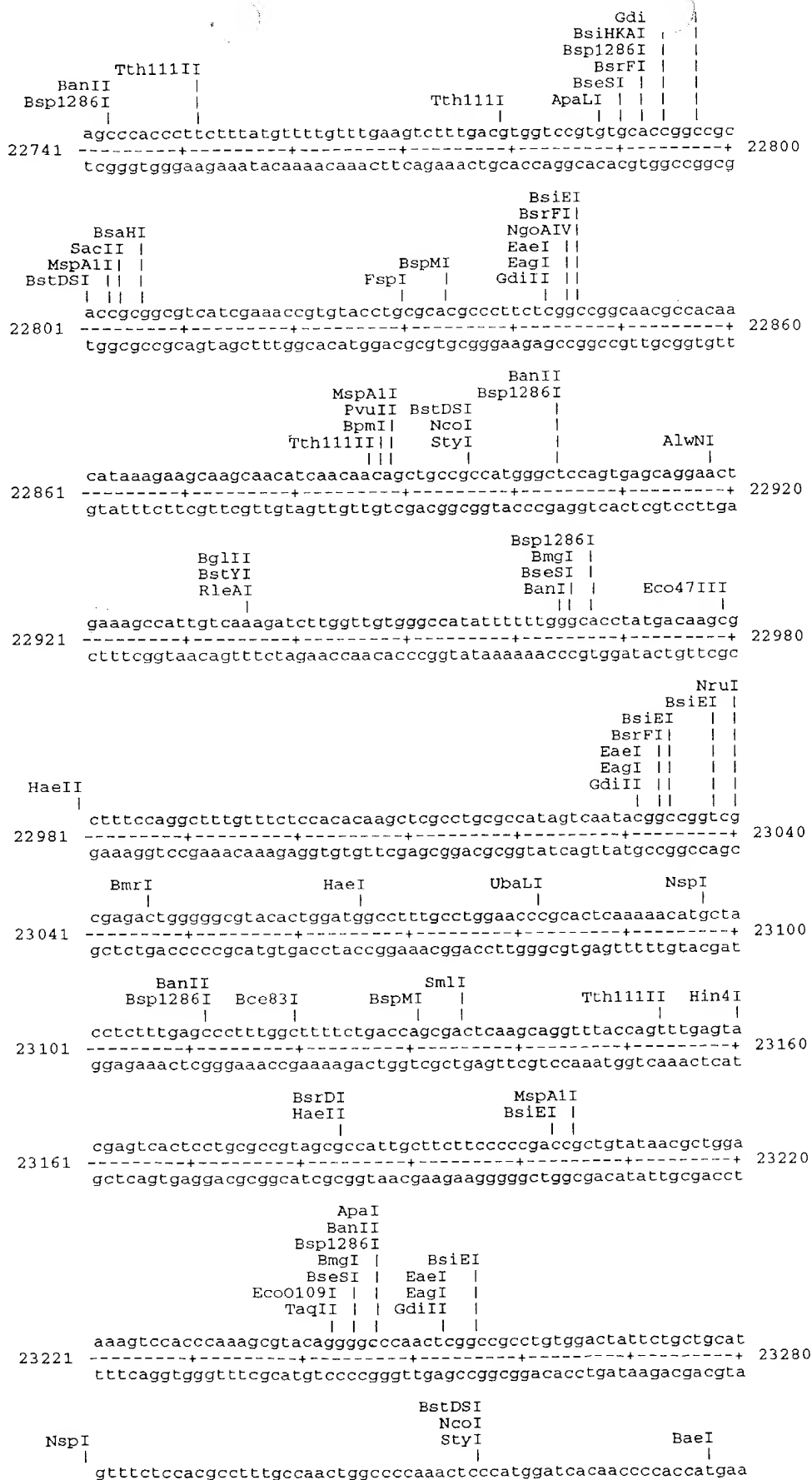


FIGURE 28

[illegible]

FIGURE 28



[illegible]

FIGURE 28

25201 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 25260  
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-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
25261 cccctctgagttcgccaccaccgctccaccgatgcgcgcaaacgcgctaccaccttccc 25320  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
ggggagactcaagcgggtggtggcggaggtggctacggcggttgcgcggtggtggaaggg  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
25321 cgtcgaggcaccctcttgaggaggaggaagtgattatcgagcaggaccaggttttgt 25380  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
gcagctccgtggggcgaaactctctctcttcaactaataagctcgtcctgggtccaaaaca  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
25381 aagcgaagacgacgaggaccgctcagtaccaacagaggataaaaagcaagaccaggacaa 25440  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
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-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
25441 cgagaggcaaacgaggaacaagtgcggcggggggacgaaaggcatggcgactacctaga 25500  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
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-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
25501 tgtgggagacgacgtgctgttgaagcatctgcagcgccagtgcgccattatctgcgacgc 25560  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
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-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
25561 gttgcaagagcgcagcgatgtgccccctcgccatagcggatgtcagccttgccctacgaacg 25620  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
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-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
25621 ccacctattctcaccgcgctaccccccaaacgccaagaaaacggcacatgcgagcccaa 25680  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
ggtggataagagtggcgcgcatggggggtttgcggttcttttgcggtgtacgctcgggtt  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
25681 cccgcgctcaacttctaccccgatttgcggtgcccagaggtgcttgcacctatcacat 25740  
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ggcgcgagggtgaagatggggcataaacggcacggtctccacgaacggtggatagtgtat  
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25741 ctttttccaaaactgcaagataccctatcctgcggtgccaacgcgagccgagcggacaa 25800  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
gaaaaaggttttgacgttctatggggataggacggcacggttggcgctcggctcgctgtt  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
25801 gcagctggccttgccgagggcgctgtcataacctgatatcgctcgctcaacgaagtgcc 25860  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
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25861 aaaaatctttgagggctcttgacgcgacgagaagcgcgcggaacgctctgcaacagga 25920  
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25921 aaacagcgaaaatgaaagtcactctggagtggttggtggaactcgaggggtgacaacgcgcg 25980  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
tttgcgcttttactttcagtgagacctcacaacaccttgagctccactggttgcgcg  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+  
Bg1I

FIGURE 28



26581 -----+-----+-----+-----+-----+ 26640  
 cgttttgaactt cggatacctgcccgaagttgctcgcgaggcaccggcgctggaccg  
 EcoNI AlwNI  
 26641 ggacatcattttccccgaacgctgttataaaccttgcaacagggtctgccagacttcac 26700  
 cctgtagtaaaaggggcttgcggacgaattttgggacgttgtcccagacggtctgaagtg  
 Bpu10I  
 HaeII  
 NspI Eco47III  
 26701 cagtcaaagcatgttgcagaacttttaggaactttatcctagagcgctcaggaatcttgcc 26760  
 gtcagtttctgtacaacgtcttgaaatccttgaaataggatctcgcgagtccttagaacgg  
 BsiHKA I  
 Bsp1286I  
 BseSI  
 BspMI  
 AarI ApaLI  
 Bsp1286I  
 BmgI  
 BseSI  
 EciI  
 BsmI  
 26761 cgccacctgctgtgcacttccttagcgactttgtgcccattaagtaccgcgaatgcctcc 26820  
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 NheI  
 PstI  
 BtsI SfcI  
 26821 gccgctttggggccactgctaccttctcgagctagccaactaccttgccctaccactctga 26880  
 cggcgaaaccccggtgacgatggaagacgtcgatcggttgatggaacggatggtgagact  
 BsrBI  
 BbsI  
 AccI  
 BstAPI  
 BpmI  
 26881 cataatggaagacgtgagcggtgacggtctactggagtgtcactgtcgctgcaacctatg 26940  
 gtattaccttctgcactcgccactgcccagatgacctcacagtgcagcgacgttggtgatac  
 BsrBI  
 MspAII  
 PvuII  
 AceIII  
 BanI  
 26941 caccgcgcacgctccctgggtttgcaattcgagctgcttaacgaaagtcaaattatcgg 27000  
 gtggggcggtggcgagggaccacacgttaagcgtcgacgaattgcttccagtttaatagcc  
 SacII  
 MspAII  
 BstDSI  
 AhdI  
 HaeIV  
 Hin4I  
 KpnI SfcI  
 27001 tacctttgagctgcaggggtccctcgctgacgaaaagtcgcggtccggggttgaaact 27060  
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 AatII  
 BsaHI  
 ApoI  
 Bsu36I  
 27061 cactccggggctgtggacgtcggttaccttcgcaaatgttacctgaggactaccacgc 27120  
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 Pfl1108I  
 BssSI  
 UbaLI  
 BbsI  
 27121 ccacgagattaggttctacgaagaccaatccccggcccaaatgcccagcttaccgcctg 27180  
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 MunI  
 HaeI  
 MscI  
 EaeI  
 BstXI  
 27181 cgtcattaccaggggccacattcttggccaattgcaagccatcaacaaagcccgccaaga 27240  
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 AhdI  
 HaeIV  
 Hin4I  
 Pfl1108I  
 BanII  
 BsiHKA I  
 Bsp1286I  
 SacI  
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FIGURE 28





SfcI BsgI BsrFI SgrAI MspAI  
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 EaeI GdiII BsiEI BsaWI  
 MspAI MspAI  
 27901 gcagcggcagcaacagcagcggccacacagaagcaaggcgaccggatagcaagactctg 27960  
 cgtcgccgctcgttgtcgtcgccggtgtgtcttcgtttccgctggcctatcgttctgagac  
 BsaHI NarI BanI BseRI  
 BseRI HaeII Eco47III  
 MspAI  
 27961 acaaagcccaagaaatccacagcggcgccagcagcaggaggagcgctgcgtctggcg 28020  
 tgtttcgggttcttttaggtgtcgccgcccgtcgtcgtcctcctcctcgacgcagaccgc  
 HaeII  
 28021 cccaacgaaccgctatcgaccgcgagcttagaaacaggatttttccactctgtatgct 28080  
 gggttgcttgggcatagctggcgccgcgaatcttgcctaaaaagggtgagacatacga  
 AceIII BsaI  
 28081 atatttcaacagagcaggggccaagaacaagagctgaaaataaaaaacaggctctcgcga 28140  
 tataaagttgtctcgtcccccgttcttgttctcgaactttatttttgcagagacgct  
 MspAI PvuII Eco57I  
 28141 tccctcaccgcgagctgcctgtatcacaaaagcgaagatcagcttcggcgccagctggaa 28200  
 agggagtgggcgctcgacggacatagtggttttcgcttctagtcgaagccgctgcgacctt  
 BbsI EarI BssHII AflII SmlI SpeI  
 28201 gacgcggaggctctcttcagtaatactgcgcgctgactcttaaggactagtttcgcgcc 28260  
 ctgcgcctccgagagaagtcatttatgacgcgcgactgagaattcctgatcaaagcgccg  
 HaeII BsaHI NarI BanI  
 EaeI GdiII Bsp24I  
 ApoI BpmI BsaXI MspAI  
 28261 ctttctcaaatttaagcgcgaaaactacgtcatctccagcggccacacccggcgccagca 28320  
 gaaagagtttaaatccgcgcttttgatgcagtagaggtcgccggtgtgggcccgcggtcgt  
 AlwNI HaeII Bsp24I ApoI AflIII BspLU11I NspI  
 28321 cctgtcgtcagcgccatttatgagcaaggaaattcccacgccctacatgtggagtaccag 28380  
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 AceIII BpmI  
 28381 ccacaaatgggacttgccggtggagctgcccagactactcaaccgaataaactacatg 28440  
 ggtgtttaccctgaacgcgcacctcgacgggttctgatgagttgggcttatttgatgtac  
 HincII RleAI  
 Eco0109I Psp5II SmaI  
 SanDI EcoRV ApoI EcoRI  
 28441 agcgcgggacccacatgatatccgggtcaacggaatccgcgcccaccgaaaccgaatt 28500  
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FIGURE 28



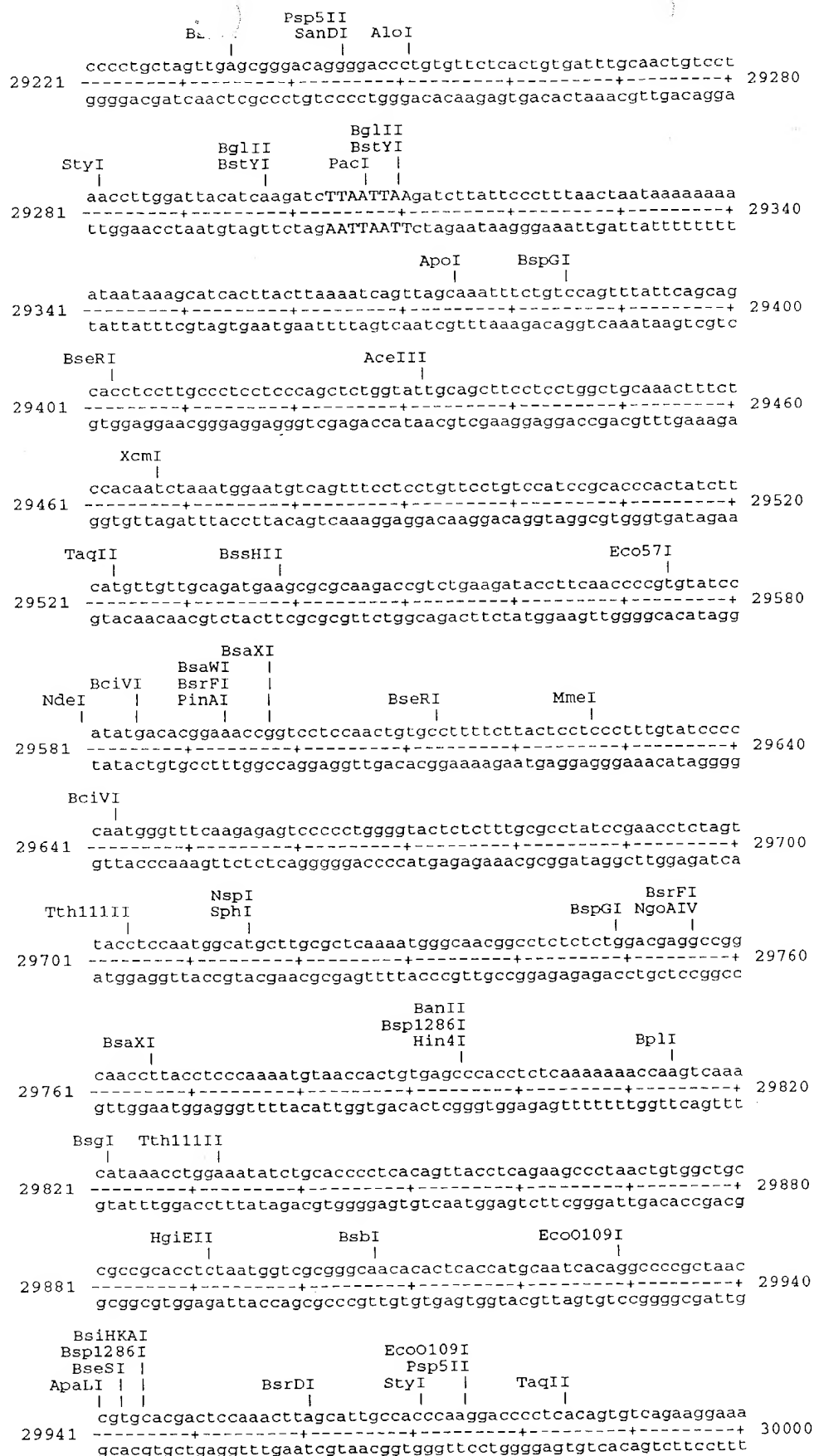


FIGURE 28

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 30061 tgcctcaccctcctaactactgccactggttagcttgggcattgacttgaaagagcccat 30120  
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 30121 ttatacacaaaatggaaaactaggactaaagtacggggctcctttgcatgtaacagacga 30180  
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 30181 cctaaacactttgaccgtagcaactggtccagggtgactattaataacttcccttgca 30240  
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 30241 aactaaagttactggagccttgggttttgattcacaaggcaatatgcaacttaattgtagc 30300  
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 30361 tgatgctcaaaaccaactaaatctaagactaggacagggccctctttttataaactcagc 30420  
 actacgagtttttggttgatttagattctgacccgtgccccgggagaaaaatatttgagtcg  
 30421 ccacaacttggaatattaactacaacaaaggcctttacttggtttacagcttcaacaattc 30480  
 ggtggtgaacctataattgatgtgttttcggaaatgaacaaatgtcgaagtttggttaag  
 30481 caaaaagcttgaggttaacctaaagcaactgccaaggggttgatgtttgacgctacagccat 30540  
 gtttttcgaactccaattggattcgtgacggttccccaactacaaactgcgatgtcggta  
 30541 agccattaatgcaggagatgggcttgaatttggttcacctaatgcaccaaacacaaatcc 30600  
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 30601 cctcaaaaacaaaattggccatggcctagatttgattcaaacaaaggctatggttccctaa 30660  
 ggagttttgttttaaccgggtaccggatccttaactaagtttgttccgataccaaggatt  
 30661 actaggaactggccttagttttgacagcacaggtgccattacagtaggaacacaaaataa 30720  
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Restriction sites (from top to bottom):  
 NheI, Tth111II, BclI, XcmI, BanII, Bsp1286I, NspI, BspGI, VspI, StyI, BpmI, Hin4I, BsaHI, ApaI, BanII, Bsp1286I, BmgI, BseSI, EcoO109I, EcoO109I, PflMI, RleAI, HaeI, StuI, SmlI, Bpu10I, StyI, Tth111II, HincII, Bce83I, BtsI, SfcI, HindIII, HpaI, VspI, ApoI, DrdII, BstDSI, NcoI, StyI, HaeI, MscI, Tth111II, EaeI, HaeI, ApoI, Tth111II, DrdII, EcoNI, HaeI, BanI

FIGURE 28

30721 tgataagctaactttgtggaccacaccagctccatctcctaactgttagactaaatgcaga 30780  
 actatttcgattgaaacacctggtgtggtcgaggtagaggattgacatctgattacgtct

30781 gaaagatgctaaactcacttttggctttaacaaaatgtggcagtcataacttgctacagt 30840  
 ctttctacgatttgagtgaaaccagaattgttttacaccgtcagtttatgaacgatgtca

30841 ttcagttttggctgttaaaggcagtttggctccaatatctggaacagttcaaagtgtctca 30900  
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30901 tcttattataagatttgacgaaaatggagtgctactaacaattccttctcggaccacaga 30960  
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30961 atattggaacttttagaaatggagatcttactgaaggcacagcctatacaaacgctgttgg 31020  
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31021 atttatgcctaacctatcagcttatccaaaatctcacggtaaaactgccaaaagtaacat 31080  
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31081 tgtcagtcagtttactttaaacggagacaaaactaaacctgtaacactaaccattacact 31140  
 acagtcagttcaaatgaatttgctctgttttgatttggacattgtgattggtaattgtga

31141 aaacgggtacacaggaacaggagacacaactccaagtgcatactctatgtcattttcatg 31200  
 tttgccatgtgtcctttgtcctctgtgttgaggttcacgtatgagatacagtaaaagta

31201 ggactggtctggccacaactacattaatgaaatatttggcacatcctcttacactttttc 31260  
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31261 atacattgccaagaataaagaatcggtttgtgttatgtttcaacgtgtttatttttcaat 31320  
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31321 tgcagaaaaatttcaagtcatttttcatcagtagtatagccaccaccacatagcttat 31380  
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31381 acagatcacccgtaccttaatacaactcacagaacctagtagttcaacctgccacctccct 31440  
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31441 cccaacacacagagtacacagtccttttctccccggctggccttaaaaagcatcatatcat 31500  
 gggttgtgtgtctcatgtgtcaggaaagaggggcccgaacggaatttttcgtagtatagta

31501 gggtaacagacatatctttaggtgttatattccacacgggttctctgtcgagccaaacgct 31560  
 cccattgtctgtataagaatccacaatataaggtgtgccaaggacagctcgggtttgcga

31561 catcagtgatattaataaactccccgggcagctcacttaagttcatgtcgctgtccagct 31620

FIGURE 28



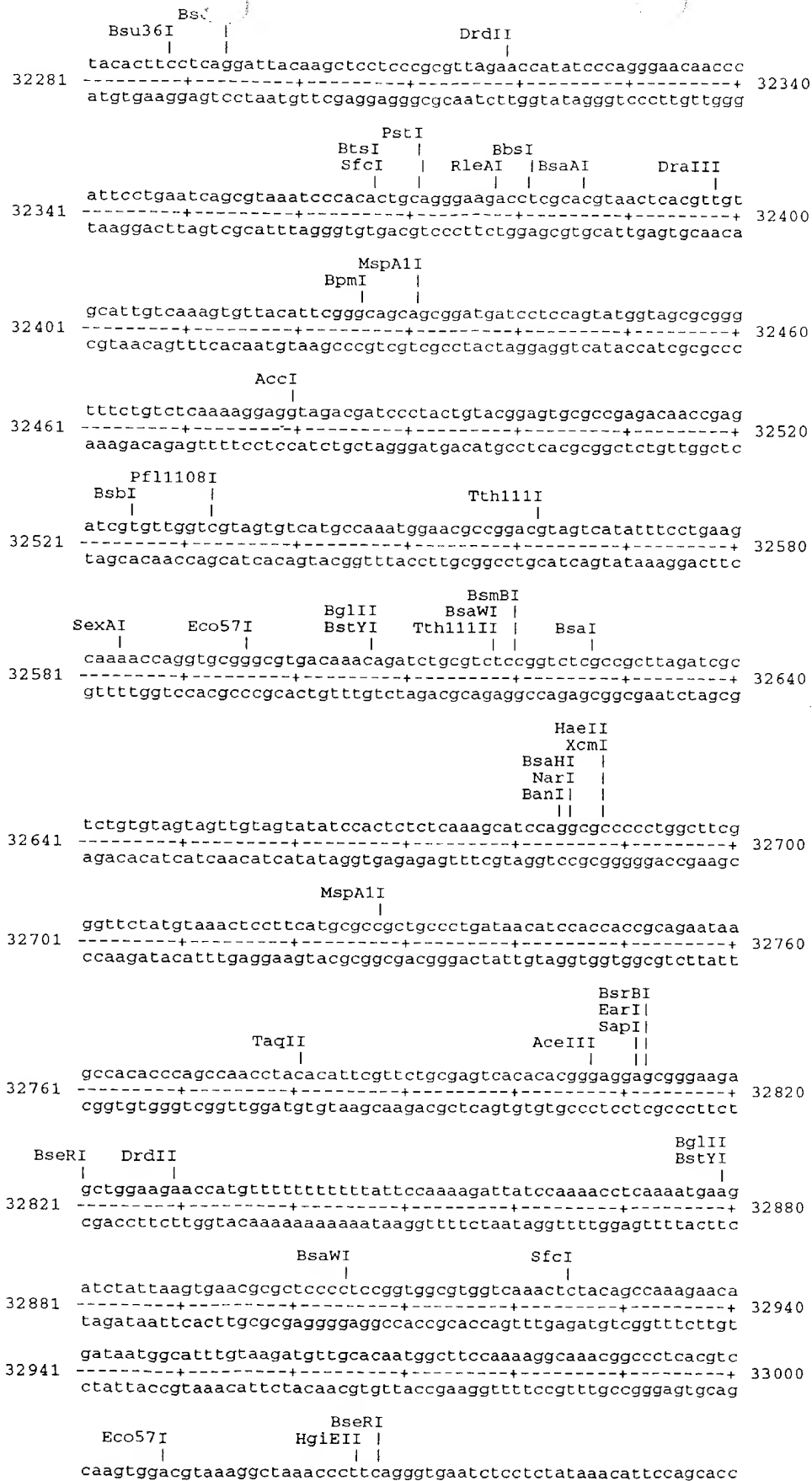


FIGURE 28

33001 -----+-----+-----+-----+-----+ 33060  
gttcacctgca cccgatttgggaagtcccacttagaggagatatttctaaggtcgcgg  
33061 -----+-----+-----+-----+-----+ 33120  
ttcaaccatgcccataaattctcatctcgccaccttctcaatatctcttaagcaaatc  
aagttggtacgggtttattaagagtagagcgggtggaagagttatatagagattcgttttag

BpmI  
EaeI  
SspI GdiII Eco57I Bce83I HaeII SmlI  
33121 -----+-----+-----+-----+-----+ 33180  
ccgaatattaagtcggccatttgtaaaaatctgctccagagcgcctccaccttcagcct  
ggcttataattcaggccggtaacatttttagacgaggtctcgcgagggtggaagtgcga

Tth111II  
RcaI ApoI  
33181 -----+-----+-----+-----+-----+ 33240  
caagcagcgaatcatgattgcaaaaattcaggttcctcacagacctgtataagattcaaa  
gttcgtcgcttagtactaacgtttttaagccaaggagtgctcgacatattctaaagttt

EcoO109I MspAII BsgI  
Psp5II PvuII BspMI  
33241 -----+-----+-----+-----+-----+ 33300  
agcggaaacattaacaaaaataccgagatcccgtaggtcccttcgcagggccagctgaaca  
tcgccttgtaattgtttttatggcgctagggcatccagggaagcgtcccggtcgacttgt

EaeI  
GdiII  
MslI BsgI  
33301 -----+-----+-----+-----+-----+ 33360  
taatcgtgcaggtctgcacggaccagcgccggaacttccccgcaggaaccttgacaaaa  
attagcacgtccagacgtgcctggctcgccggtgaaggggaggtccttggaactgtttt

RleAI  
33361 -----+-----+-----+-----+-----+ 33420  
gaaccacactgattatgacacgcataactcggagctatgctaaccagcgtagccccgatg  
cttgggtgtgactaataactgtgcgtatgagcctcgatacgattggtcgcatcggggctac

HindIII  
33421 -----+-----+-----+-----+-----+ 33480  
taagctttgttgcattggcgccgatataaaatgcaaggtgctgctcaaaaaatcaggcaa  
attcgaaacaacgtacccgccgtatattttacgttcacgacgagtttttagtcggtt

Pfl1108I MslI BspMI  
33481 -----+-----+-----+-----+-----+ 33540  
agcctcgcgcaaaaaaagaaagcacatcgtagtcatgctcatgcagataaaggcaggttaag  
tcggagcgcggttttttcttctgtagcatcagtagttagctattttccgtccattc

BsaWI  
BspEI DrdII  
AflIII  
BspLUII NspI  
33541 -----+-----+-----+-----+-----+ 33600  
ctccggaaccaccacagaaaaagacaccatttttctctcaaacatgtctcggggtttctg  
gaggccttggtggtgtctttttctgtggttaaaaagagagtttgtagacagcggccaaagac

DraI  
33601 -----+-----+-----+-----+-----+ 33660  
cataaacacaaaaataaaataacaaaaaacatttaaacattagaagcctgtcttacaaca  
gtatttgtgttttattttattgttttttgtaaatgttaattcttcggacagaaatgttgt

BglI  
EaeI BsrFI  
GdiII NgoAIV  
33661 -----+-----+-----+-----+-----+ 33720  
ggaaaaaacaacccttataagcataagacggactacggccatgcccgtgaccgtaaaaa  
cctttttgttggaatatctgtattctgctgatgcgggtacggccgactggcattttt

TaqII  
BseRI Hin4I AceIII  
BsaWI  
BspEI  
33721 -----+-----+-----+-----+-----+ 33780  
aactgggtcaccgtgattaaaaagcaccccgacagctcctcggtcatgtccggagtcata  
ttgaccagtggcactaatttttctggtgggtgtcagaggagccagtagcaggtcagtat

TaqII BsiEI  
33781 -----+-----+-----+-----+-----+ 33840  
atgtaagactcggtaaacacatcaggttgattcatcggtcagtgctaaaaagcgacgaa  
tacattctgagcattttgtgtagtccaactaagtagccagtcacgatttttctgctggctt

FIGURE 28



TaqII  
 SmaI  
 Aval  
 33841 atagcccggggaatacatacccgaggcgtagagacaacattacagcccccataggagg 33900  
 taccgggcccccttatgtatgggcgtccgcatctctgttgtaatgtcgggggtatcctcc  
 VspI  
 AvrII  
 StyI  
 33901 tatacaaaaattaataggagagaaaaacacataaacacctgaaaaacccctcctgcctagg 33960  
 atattgttttaattactctctttttgtgtatttggacttttgggaggacggatcc  
 HaeII  
 BpmI BsrBI Eco47III MspAII  
 33961 caaaatagcacccctcccgctccagaacaacatacagcgcttcacagcggcagcctaacag 34020  
 gttttatcgtgggagggcgagggtcttgtgtatgtcgcgaagtgtcgccgtcggattgtc  
 BanI  
 34021 tcagccttaccagtaaaaaagaaaacctattaaaaaacaccactcgacacggcaccagc 34080  
 agtcggaatgggtcattttttcttttggataattttttgtggtgagctgtgcggtggtcg  
 AceIII BsgI  
 34081 tcaatcagtcacagtgtaaaaaaggccaagtgcagagcgagtatatataggactaaaaa 34140  
 agttagtcagtggtcacattttttcccggttcacgtctcgctcatatatatcctgattttt  
 TaqII  
 34141 atgacgtaacgggttaaagtcacaaaaaacacccagaaaaccgcacgcaacctacgccc 34200  
 tactgcattgccaatttcagggtgtttttgtgggtcttttggcgtgcgcttggtatgctggg  
 RleAI  
 34201 agaaacgaaagccaaaaaacccacaacttctcctcaaatcgtcacttccggttttcccacgtt 34260  
 tctttgctttcggttttttgggtgttgaaggagtttagcagtgaaaggcaaaagggtgcaa  
 BsaAI  
 SnaBI BsbI EciI  
 34261 acgtaacttcccatttttaagaaaactacaattcccaacacatacaagttactccgccta 34320  
 tgcattgaagggttaaaattctttttagtgtaagggttggtgtatgttcaatgaggcgggat  
 34321 aaacctacgtcaccgcggcccggttcccacgccccgcgcacgtcacaaactccacccctc 34380  
 tttggatgcagtgggcggggcaagggtgccccggcgcggtgcagtggtttgaggtgggggag  
 34381 attatcatattggcttcaatccaaaataagggtatattattgatgatg 34427  
 taatagtataaccgaagttaggtttttatccatataataactactac

#### Enzymes that do cut:

|          |          |        |        |          |          |          |          |
|----------|----------|--------|--------|----------|----------|----------|----------|
| AarI     | AatII    | AccI   | AceIII | AcII     | AflII    | AflIII   | AhdI     |
| AloI     | AlwNI    | ApaI   | ApalI  | ApoI     | AscI     | AvaI     | AvrII    |
| BaeI     | BamHI    | BanI   | BanII  | BbsI     | BbvCI    | Bce83I   | BcgI     |
| BciVI    | BclI     | BglI   | BglII  | BmgI     | BmrI     | BplI     | BpmI     |
| Bpu10I   | Bpu1102I | BsaI   | BsaAI  | BsaBI    | BsaHI    | BsaWI    | BsaXI    |
| BsbI     | BseRI    | BseSI  | BsgI   | BsiEI    | BsiHKAI  | BsmI     | BsmBI    |
| Bsp24I   | Bsp1286I | BspEI  | BspGI  | BspLU11I | BspMI    | BsrBI    | BsrDI    |
| BsrFI    | BsrGI    | BssHII | BssSI  | BstAPI   | BstDSI   | BstEII   | BstXI    |
| BstYI    | BstZ17I  | Bsu36I | BtsI   | ClaI     | DraI     | DraIII   | DrDI     |
| DrdII    | EaeI     | EagI   | EaRI   | EciI     | Eco47III | Eco57I   | EcoNI    |
| EcoO109I | EcoRI    | EcoRV  | FseI   | FspI     | GdiII    | HaeI     | HaeII    |
| HaeIV    | HgiEII   | Hin4I  | HincII | HindIII  | HpaI     | KpnI     | MluI     |
| MmeI     | MscI     | MslI   | MspAII | MunI     | NarI     | NcoI     | NdeI     |
| NgoAIV   | NheI     | NotI   | NruI   | NsiI     | NspI     | PacI     | Pfl1108I |
| PflMI    | PinAI    | PmeI   | PmlI   | PshAI    | Psp5II   | PstI     | PvuI     |
| PvuII    | RcaI     | RleAI  | RsrII  | SacI     | SacII    | SalI     | SanDI    |
| SapI     | SbfI     | ScaI   | SexAI  | SfcI     | SfiI     | SgfI     | SgrAI    |
| SmaI     | SmlI     | SnaBI  | SpeI   | SphI     | SrfI     | Sse8647I | SspI     |
| StuI     | StyI     | SunI   | SwaI   | TaqII    | TatI     | Tth111I  | Tth111II |
| UbaLI    | VspI     | XbaI   | XcmI   | XhoI     | XmnI     |          |          |

#### Enzymes that do not cut:

NspV

FIGURE 28

33001 -----+-----+-----+-----+-----+-----+-----+ 33060  
 gttcacctgc...ccgatttgggaagtcccaacttagaggagatatattgtaaggtcgcgg  
 33061 -----+-----+-----+-----+-----+-----+-----+ 33120  
 ttcaacctatgcccataaattctcatctcgccaccttctcaatatatctctaagcaaatc  
 aagttggtagcgggtttattaagagtagagcgggtggaagagttatatagagattcgttttag

BpmI  
 EaeI |  
 SspI | GdiII | Eco57I | Bce83I | SmlI |  
 HaeII |  
 33121 -----+-----+-----+-----+-----+-----+-----+ 33180  
 ccgaatattaagtcggccattgttaaaaatctgctccagagcgcctccaccttcagcct  
 ggcttataattcaggccggtaacatttttagacgaggtctcgcgagggtggaagtccga

Tth111II  
 RcaI | ApoI |  
 33181 -----+-----+-----+-----+-----+-----+-----+ 33240  
 caagcagcgaatcatgattgcaaaaattcaggttcctcacagacctgtataagattcaaa  
 gttcgtagcttagtactaacgtttttaagccaaggagtgctggacatatcttaagttt

Eco0109I | MspAII | BsgI |  
 Psp5II | PvuII | BspMI |  
 33241 -----+-----+-----+-----+-----+-----+-----+ 33300  
 agcggaaacattaacaaaaataccgcgatcccgtaggtcccttcgcagggccagctgaaca  
 tcgccttgtaattgtttttatggcgctaggcatccagggaagcgtcccggtcgacttgt

EaeI |  
 GdiII |  
 MslI | BsgI |  
 33301 -----+-----+-----+-----+-----+-----+-----+ 33360  
 taatcgtgcaggtctgcacggaccagcgcggccacttccccgccaggaaccttgacaaaa  
 attagcacgtccagacgtgcctggtcgcgccgggtgaagggcggtccttggaactgtttt

RleAI |  
 33361 -----+-----+-----+-----+-----+-----+-----+ 33420  
 gaaccacactgattatgacacgcatactcggagctatgctaaccagcgtagccccgatg  
 cttgggtgtgactaataactgtgcgtatgagcctcgatacagattggtcgcatcggggtac

HindIII |  
 33421 -----+-----+-----+-----+-----+-----+-----+ 33480  
 taagctttgttgcattggcgccgatataaaatgcaaggtgctgctcaaaaaatcaggcaa  
 attcgaaacaacgtacccgcgctatatattttagcttcacgagagtttttttagtccgtt

Pfl1108I | MslI | BspMI |  
 33481 -----+-----+-----+-----+-----+-----+-----+ 33540  
 agcctcgcgcaaaaaaagaagacacatcgtagtcatgctcatgcagataaaggcaggttaag  
 tcggagcgcgtttttttcttctgtgtagcatcagtagttagtctatttccgtccattc

BsaWI | NspI |  
 BspEI | DrdII | AflIII | BspLU11I | Tth111II |  
 33541 -----+-----+-----+-----+-----+-----+-----+ 33600  
 ctccggaaccaccacagaaaaagacaccatttttctctcaaacatgtctcggggtttctg  
 gaggccttggtggtgtctttttctgtggtaaaaagagagtttgtagacagcggccaaagac

DraI |  
 33601 -----+-----+-----+-----+-----+-----+-----+ 33660  
 cataaacacaaaaataaaataacaaaaaacattttaaacattagaagcctgtcttacaaca  
 gtattttgtgttttattttattgttttttgtaaatttgaattcttcggacagaatgttgt

BglI |  
 EaeI | BsrFI |  
 GdiII | NgoAIV |  
 33661 -----+-----+-----+-----+-----+-----+-----+ 33720  
 ggaaaaaacaaccttataagcataagacggactacggccatgccggcgtgaccgtaaaaa  
 cctttttgttggaatatctgtattctgctgtatgccggtacggccgactggcattttt

TaqII | BsaWI |  
 BseRI | Hin4I | AceIII | BspEI |  
 33721 -----+-----+-----+-----+-----+-----+-----+ 33780  
 aactgggtcacggtgattaaaaagcaccaccgacagctcctcggtcatgtccggagtcata  
 ttgaccagtgggcactaatttttctggtggtggtgtcgaggagccagtagcaggtcctcagtat

TaqII | BsiEI |  
 33781 -----+-----+-----+-----+-----+-----+-----+ 33840  
 atgtaagactcggtaaacacatcaggttgattcatcggtcagtgctaaaaagcgaccgaa  
 tacattctgagccatttgtgtagtccaactaagtagccagtcagatttttctgctggctt

FIGURE 28